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(54) Title: NOVEL COMPOUNDS			
(57) Abstract <p>This invention relates to newly identified polynucleotides, polypeptides encoded by such polynucleotides, the uses of such polynucleotides and polypeptides, as well as the production of such polynucleotides and polypeptides and recombinant host cells transformed with the polynucleotides. This invention also relates to inhibiting the biosynthesis or action of such polynucleotides or polypeptides and to the use of such inhibitors in therapy.</p>			

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NOVEL COMPOUNDS

Field of the Invention:

This invention relates to newly identified polynucleotides, polypeptides encoded by such polynucleotides, the uses of such polynucleotides and polypeptides, as well as the
5 production of such polynucleotides and polypeptides and recombinant host cells transformed with the polynucleotides. This invention also relates to inhibiting the biosynthesis or action of such polynucleotides or polypeptides and to the use of such inhibitors in therapy. Preferred embodiments of the invention include Streptococcal polypeptides and polynucleotides, particularly those of *Streptococcus pneumoniae*.

10 Background of the Invention:

The Streptococci make up a medically important genera of microbes known to cause several types of disease in humans, including otitis media, pneumonia and meningitis. Since its isolation more than 100 years ago, *Streptococcus pneumoniae* has been one of the more intensively studied microbes. For example, much of our early understanding that
15 DNA is, in fact, the genetic material was predicated on the work of Griffith and of Avery, Macleod and McCarty using this microbe. Despite the vast amount of research with *S. pneumoniae*, many questions concerning the virulence of this microbe remain.

While certain Streptococcal factors associated with pathogenicity have been identified, e.g., capsule polysaccharides, peptidoglycans, pneumolysins, PspA Complement
20 factor H binding component, autolysin, neuraminidase, peptide permeases, hydrogen peroxide, IgA1 protease, the list is certainly not complete. Further very little is known concerning the temporal expression of such genes during infection and disease progression in a mammalian host. Discovering the sets of genes the bacterium is likely to be expressing at the different stages of infection, particularly when an infection is established, provides
25 critical information for the screening and characterization of novel antibacterials which can interrupt pathogenesis. In addition to providing a fuller understanding of known proteins, such an approach will identify previously unrecognised targets.

Brief Description of the Invention:

This invention provides novel proteins, particularly those from *Streptococcus*
30 *pneumoniae*, strain 0100993, characterised in that it comprises the amino acid sequences given herein or fragments, analogues or derivatives thereof.

In accordance with another aspect of the present invention, there are provided polynucleotides (DNA or RNA) which encode such polypeptides.

In particular the invention provides polynucleotides having the DNA sequences given herein.

5 The invention also relates to novel oligonucleotides derived from the sequences given herein which can act as PCR primers in the process herein described to determine whether or not the *Streptococcus pneumoniae* gene identified herein in whole or in part is expressed in infected tissue. It is recognised that such sequences will also have utility in diagnosis of the stage of infection and type of infection the pathogen has attained. The proteins so identified are also useful as targets in screens designed to identify antimicrobial compounds.

10 It is an object of the invention to provide polypeptides that have been identified as novel polypeptides by homology between the amino acid sequence set out in the Sequence Listing and a known amino acid sequence or sequences of other proteins such as the proteins identified under the heading Identity in Table 1.

15 It is a further object of the invention to provide polynucleotides that encode polypeptides set forth in the Sequence Listing, particularly polynucleotides that encode the polypeptide set forth in the Sequence Listing.

In a particularly preferred embodiment of the invention the polynucleotide comprises a region encoding polypeptides comprising the sequence set out in the Sequence Listing, or a variant thereof.

20 In another particularly preferred embodiment of the invention there is a novel protein from comprising an amino acid sequence of the Sequence Listing, or a variant thereof.

25 In accordance with another aspect of the invention, there is provided the use of a polynucleotide of the invention for therapeutic or prophylactic purposes, in particular genetic immunization. Among the particularly preferred embodiments of the invention are naturally occurring allelic variants the polynucleotides set forth in the Sequence Listing and polypeptides encoded thereby.

In accordance with yet another aspect of the invention, there are provided inhibitors to such polypeptides, useful as antibacterial agents, including, for example, antibodies.

30 In accordance with certain preferred embodiments of the invention, there are provided products, compositions and methods for assessing expression of the sequences the Sequence Listing, treating disease, for example, otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema and endocarditis, and most particularly meningitis, such as for example infection of cerebrospinal fluid, assaying genetic variation, and

administering a polypeptide or polynucleotide of the invention to an organism to raise an immunological response against a bacteria, especially a *Streptococcus pneumoniae* bacteria.

In accordance with certain preferred embodiments of this and other aspects of the invention there are provided polynucleotides that hybridize to polynucleotide sequences of the invention, particularly under stringent conditions.

In certain preferred embodiments of the invention there are provided antibodies against polypeptides of the invention.

In other embodiments of the invention there are provided methods for identifying compounds which bind to or otherwise interact with and inhibit or activate an activity of a polypeptide or polynucleotide of the invention comprising: contacting a polypeptide or polynucleotide of the invention with a compound to be screened under conditions to permit binding to or other interaction between the compound and the polypeptide or polynucleotide to assess the binding to or other interaction with the compound, such binding or interaction being associated with a second component capable of providing a detectable signal in response to the binding or interaction of the polypeptide or polynucleotide with the compound; and determining whether the compound binds to or otherwise interacts with and activates or inhibits an activity of the polypeptide or polynucleotide by detecting the presence or absence of a signal generated from the binding or interaction of the compound with the polypeptide or polynucleotide.

In accordance with yet another aspect of the invention, there are provided agonists and antagonists of the polynucleotide and/or polypeptides of the invention, preferably bacteriostatic or bacteriocidal agonists and antagonists.

In a further aspect of the invention there are provided compositions comprising a polynucleotide or a polypeptide of the invention for administration to a cell or to a multicellular organism.

Various changes and modifications within the spirit and scope of the disclosed invention will become readily apparent to those skilled in the art from reading the following descriptions and from reading the other parts of the present disclosure.

Detailed Description of the Invention:

Each of the DNA sequences provided herein may be used in the discovery and development of antibacterial compounds. Because each of the sequences contains an open reading frame (ORF) with appropriate initiation and termination codons, the encoded protein upon expression can be used as a target for the screening of antimicrobial drugs. Additionally, the DNA sequences encoding preferably the amino terminal regions of the encoded protein or the Shine-Delgarno region can be used to construct antisense sequences

to control the expression of the coding sequence of interest. Furthermore, many of the sequences disclosed herein also provide regions upstream and downstream from the encoding sequence. These sequences are useful as a source of regulatory elements for the control of bacterial gene expression. Such sequences are conveniently isolated by
5 restriction enzyme action or synthesized chemically and introduced, for example, into promoter identification strains. These strains contain a reporter structural gene sequence located downstream from a restriction site such that if an active promoter is inserted, the reporter gene will be expressed.

Although each of the sequences may be employed as described above, this
10 invention also provides several means for identifying particularly useful target genes. The first of these approaches entails searching appropriate databases for sequence matches in related organisms. Thus, if a homologue exists, the Streptococcal-like form of this gene would likely play an analogous role. For example, a Streptococcal protein identified as homologous to a cell surface protein in another organism would be useful as a vaccine
15 candidate. To the extent such homologies have been identified for the sequences disclosed herein they are reported along with the encoding sequence.

Recently techniques have become available to evaluate temporal gene expression in bacteria, particularly as it applies to viability under laboratory and infection conditions. A number of methods can be used to identify genes which are essential to survival *per se*, or
20 essential to the establishment/maintenance of an infection. Identification of an ORF unknown by one of these methods yields additional information about its function and permits the selection of such an ORF for further development as a screening target. Briefly, these approaches include:

1) Signature Tagged Mutagenesis (STM)

25 This technique is described by Hensel *et al.*, *Science* 269: 400-403(1995), the contents of which is incorporated by reference for background purposes. Signature tagged mutagenesis identifies genes necessary for the establishment/maintenance of infection in a given infection model.

The basis of the technique is the random mutagenesis of target organism by various
30 means (e.g., transposons) such that unique DNA sequence tags are inserted in close proximity to the site of mutation. The tags from a mixed population of bacterial mutants and bacteria recovered from an infected hosts are detected by amplification, radiolabeling and hybridisation analysis. Mutants attenuated in virulence are revealed by absence of the tag from the pool of bacteria recovered from infected hosts.

In Streptococcus pneumoniae, because the transposon system is less well developed, a more efficient way of creating the tagged mutants is to use the insertion-duplication mutagenesis technique as described by Morrison et al., J. Bacteriol. 159:870 (1984) the contents of which is incorporated by reference for background purposes.

5 **2) In Vivo Expression Technology (IVET)**

This technique is described by Camilli et al., Proc. Nat'l. Acad. Sci. USA. 91:2634-2638 (1994), the contents of which is incorporated by reference for background purposes.

IVET identifies genes up-regulated during infection when compared to laboratory cultivation, implying an important role in infection. ORF identified by this technique are
10 implied to have a significant role in infection establishment/maintenance.

In this technique random chromosomal fragments of target organism are cloned upstream of a promoter-less recombinase gene in a plasmid vector. This construct is introduced into the target organism which carries an antibiotic resistance gene flanked by resolvase sites. Growth in the presence of the antibiotic removes from the population those
15 fragments cloned into the plasmid vector capable of supporting transcription of the recombinase gene and therefore have caused loss of antibiotic resistance. The resistant pool is introduced into a host and at various times after infection bacteria may be recovered and assessed for the presence of antibiotic resistance. The chromosomal fragment carried by each antibiotic sensitive bacterium should carry a promoter or portion of a gene normally
20 upregulated during infection. Sequencing upstream of the recombinase gene allows identification of the up regulated gene.

3) Differential display

This technique is described by Chuang et al., J. Bacteriol. 175:2026-2036 (1993), the contents of which is incorporated by reference for background purposes. This method
25 identifies those genes which are expressed in an organism by identifying mRNA present using randomly-primed RT-PCR. By comparing pre-infection and post infection profiles, genes up and down regulated during infection can be identified and the RT-PCR product sequenced and matched to ORF 'unknowns'.

4) Generation of conditional lethal mutants by transposon mutagenesis.

This technique, described by de Lorenzo, V. *et al.*, Gene 123:17-24 (1993); Neuwald, A. F. *et al.*, Gene 125: 69-73(1993); and Takiff, H. E. *et al.*, J. Bacteriol. 174:1544-1553(1992), the contents of which is incorporated by reference for

5 background purposes, identifies genes whose expression are essential for cell viability.

In this technique transposons carrying controllable promoters, which provide transcription outward from the transposon in one or both directions, are generated. Random insertion of these transposons into target organisms and subsequent isolation of insertion mutants in the presence of inducer of promoter activity ensures that insertions which

10 separate promoter from coding region of a gene whose expression is essential for cell viability will be recovered. Subsequent replica plating in the absence of inducer identifies such insertions, since they fail to survive. Sequencing of the flanking regions of the transposon allows identification of site of insertion and identification of the gene disrupted. Close monitoring of the changes in cellular processes/morphology during growth in the

15 absence of inducer yields information on likely function of the gene. Such monitoring could include flow cytometry (cell division, lysis, redox potential, DNA replication), incorporation of radiochemically labeled precursors into DNA, RNA, protein, lipid, peptidoglycan, monitoring reporter enzyme gene fusions which respond to known cellular stresses.

20 **5) Generation of conditional lethal mutants by chemical mutagenesis.**

This technique is described by Beckwith, J., Methods in Enzymology 204: 3-18(1991), the contents of which are incorporated herein by reference for background purposes. In this technique random chemical mutagenesis of target organism, growth at temperature other than physiological temperature (permissive temperature) and subsequent

25 replica plating and growth at different temperature (e.g. 42°C to identify ts, 25°C to identify cs) are used to identify those isolates which now fail to grow (conditional mutants). As above close monitoring of the changes upon growth at the non-permissive temperature yields information on the function of the mutated gene. Complementation of conditional lethal mutation by library from target organism and sequencing of complementing gene

30 allows matching with unknown ORF.

6) RT-PCR

Streptococcus pneumoniae messenger RNA is isolated from bacterial infected tissue e.g. 48 hour murine lung infections, and the amount of each mRNA species assessed by reverse transcription of the RNA sample primed with random hexanucleotides followed by PCR

with gene specific primer pairs. The determination of the presence and amount of a particular mRNA species by quantification of the resultant PCR product provides information on the bacterial genes which are transcribed in the infected tissue. Analysis of gene transcription can be carried out at different times of infection to gain a detailed knowledge of gene regulation in bacterial pathogenesis allowing for a clearer understanding of which gene products represent targets for screens for novel antibacterials. Because of the gene specific nature of the PCR primers employed it should be understood that the bacterial mRNA preparation need not be free of mammalian RNA. This allows the investigator to carry out a simple and quick RNA preparation from infected tissue to obtain bacterial mRNA species which are very short lived in the bacterium (in the order of 2 minute half-lives). Optimally the bacterial mRNA is prepared from infected murine lung tissue by mechanical disruption in the presence of TRIzol (GIBCO-BRL) for very short periods of time, subsequent processing according to the manufacturers of TRIzol reagent and DNAase treatment to remove contaminating DNA. Preferably the process is optimised by finding those conditions which give a maximum amount of *S.pneumoniae* 16S ribosomal RNA as detected by probing Northern blots with a suitably labelled sequence specific oligonucleotide probe. Typically a 5' dye labelled primer is used in each PCR primer pair in a PCR reaction which is terminated optimally between 8 and 25 cycles. The PCR products are separated on 6% polyacrylamide gels with detection and quantification using GeneScanner (manufactured by ABI).

Each of these techniques may have advantages or disadvantage depending on the particular application. The skilled artisan would choose the approach that is the most relevant with the particular end use in mind. For example, some genes might be recognised as essential for infection but in reality are only necessary for the initiation of infection and so their products would represent relatively unattractive targets for antibacterials developed to cure established and chronic infections.

Use of the of these technologies when applied to the ORFs of the present invention enables identification of bacterial proteins expressed during infection, inhibitors of which would have utility in anti-bacterial therapy.

Streptococcus pneumoniae, strain 0100993 has been deposited at the National Collection of Industrial and Marine Bacteria Ltd. (NCIMB), Aberdeen, Scotland under NCIMB number 40794 on 11 April 1996, and a *Streptococcus pneumoniae*, strain 0100993 DNA library in *E. coli* was similarly deposited on 17 April 1996 under NCIMB number 40800.

The nucleotide sequences disclosed herein can be obtained by synthetic chemical techniques known in the art or can be obtained from *Streptococcus pneumoniae*, strain 0100993 by probing a DNA preparation with probes constructed from the particular sequences disclosed herein. Alternatively, oligonucleotides derived from a disclosed sequence can act as PCR primers in a process of PCR-based cloning of the sequence from a bacterial genomic source. It is recognised that such sequences will also have utility in diagnosis of the stage of infection and type of infection the pathogen has attained.

To obtain the polynucleotide encoding the protein using the DNA sequence given herein typically a library of clones of chromosomal DNA of *Streptococcus pneumoniae*, strain 0100993 in *E. coli* or some other suitable host is probed with a radiolabelled oligonucleotide, preferably a 17mer or longer, derived from the partial sequence. Clones carrying DNA identical to that of the probe can then be distinguished using high stringency washes. By sequencing the individual clones thus identified with sequencing primers designed from the original sequence it is then possible to extend the sequence in both directions to determine the full gene sequence. Conveniently such sequencing is performed using denatured double stranded DNA prepared from a plasmid clone. Suitable techniques are described by Maniatis, T., Fritsch, E.F. and Sambrook, J. in MOLECULAR CLONING, A Laboratory Manual, 2nd edition, 1989, Cold Spring Harbor Laboratory (see: Screening By Hybridization 1.90 and Sequencing Denatured Double-Stranded DNA Templates 13.70).

A polynucleotide of the present invention may be in the form of RNA or in the form of DNA, which DNA includes cDNA, genomic DNA, and synthetic DNA. The DNA may be double-stranded or single-stranded, and if single stranded may be the coding strand or non-coding (anti-sense) strand. The coding sequence which encodes the polypeptide may be identical to the coding sequence shown or may be a different coding sequence which coding sequence, as a result of the redundancy or degeneracy of the genetic code, encoding the same polypeptide.

The present invention includes variants of the hereinabove described polynucleotides which encode fragments, analogues and derivatives of the polypeptide characterized by the deduced amino acid sequence given herein. The variant of the polynucleotide may be a naturally occurring allelic variant of the polynucleotide or a non-naturally occurring variant of the polynucleotide. In addition to the standard A, G, C, T/U representations for nucleic acid bases, the term "N" is also used. "N" means that any of the four DNA or RNA bases may appear at such a designated position in the DNA or RNA

sequence, except that N cannot be a base that when taken in combination with adjacent nucleotide positions, when read in the correct reading frame, would have the effect of generating a premature termination codon in such reading frame.

Thus, the present invention includes polynucleotides encoding the same
5 polypeptide characterized by the deduced amino acid sequence given herein as well as variants of such polynucleotides which variants encode for a fragment, derivative or analogue of the polypeptide. Such nucleotide variants include deletion variants, substitution variants and addition or insertion variants.

The polynucleotide may have a coding sequence which is a naturally occurring
10 allelic variant of the coding sequence characterized by the DNA sequence disclosed herein. As known in the art, an allelic variant is an alternate form of a polynucleotide sequence which may have a substitution, deletion or addition of one or more nucleotides, which does not substantially alter the function of the encoded polypeptide.

The polynucleotide which encodes for the mature polypeptide, may include only
15 the coding sequence for the mature polypeptide or the coding sequence for the mature polypeptide and additional coding sequence such as a leader or secretory sequence or a proprotein sequence.

Thus, the term "polynucleotide encoding a polypeptide" encompasses a
polynucleotide which includes only coding sequence for the polypeptide as well as a
20 polynucleotide which includes additional coding and/or non-coding sequence.

The present invention therefore includes polynucleotides, wherein the coding
sequence for the mature polypeptide may be fused in the same reading frame to a
polynucleotide sequence which aids in expression and secretion of a polypeptide from a
host cell, for example, a leader sequence which functions as a secretory sequence for
25 controlling transport of a polypeptide from the cell. The polypeptide having a leader
sequence is a preprotein and may have the leader sequence cleaved by the host cell to form
the mature form of the polypeptide. The polynucleotides may also encode for a proprotein
which is the mature protein plus additional 5' amino acid residues. A mature protein having
a prosequence is a proprotein and may be an inactive form of the protein. Once the
30 prosequence is cleaved an active mature protein remains.

Thus, for example, the polynucleotide of the present invention may code for a
mature protein, or for a protein having a prosequence or for a protein having both a
prosequence and a presequence (leader sequence). Further, the amino acid sequences
provided herein show a methionine residue at the NH₂-terminus. It is appreciated, however,

that during post-translational modification of the peptide, this residue may be deleted.

Accordingly, this invention contemplates the use of both the methionine-containing and the methionineless amino terminal variants of each protein disclosed herein.

5 The polynucleotides of the present invention may also have the coding sequence fused in frame to a marker sequence at either the 5' or 3' terminus of the gene which allows for purification of the polypeptide of the present invention. The marker sequence may be a hexa-histidine tag supplied by the pQE series of vectors (supplied commercially by Quiagen Inc.) to provide for purification of the polypeptide fused to the marker in the case of a bacterial host.

10 The present invention further relates to polynucleotides which hybridize to the hereinabove-described sequences if there is at least 50% and preferably at least 70% identity between the sequences. The present invention particularly relates to polynucleotides, particularly Streptococcal polynucleotides, which hybridize under stringent conditions to the hereinabove-described polynucleotides. As herein used, the term "stringent conditions"

15 means hybridization will occur only if there is at least 95% and preferably at least 97% identity between the sequences. The polynucleotides which hybridize to the hereinabove described polynucleotides in a preferred embodiment encode polypeptides which retain substantially the same biological function or activity as the polypeptide characterised by the deduced amino acid sequence given herein. An example of stringent hybridization

20 conditions is overnight incubation at 42°C in a solution comprising: 50% formamide, 5x SSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 micrograms/ml denatured, sheared salmon sperm DNA, followed by washing the hybridization support in 0.1x SSC at about 65°C. Hybridization and wash conditions are well known and exemplified in Sambrook, *et al.*,

25 Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, N.Y., (1989), particularly Chapter 11 therein.

The invention also provides a polynucleotide consisting essentially of a polynucleotide sequence obtainable by screening an appropriate library containing the complete gene for a polynucleotide sequence selected from the group consisting of the

30 polynucleotides of the Sequence Listing under stringent hybridization conditions with a probe having the sequence of said polynucleotide sequence set forth in said polynucleotide of the Sequence Listing or a fragment thereof; and isolating said DNA sequence. Fragments useful for obtaining such a polynucleotide include, for example, probes and primers described elsewhere herein.

"Identity," as known in the art and used herein, is a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, "identity" also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match
5 between strings of such sequences. "Identity" and "similarity" can be readily calculated by known methods, including but not limited to those described in (*Computational Molecular Biology*, Lesk, A.M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D.W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data*, Part I, Griffin, A.M., and Griffin, H.G., eds.,
10 Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; and Carillo, H., and Lipman, D., *SIAM J. Applied Math.*, 48: 1073 (1988). Preferred methods to determine identity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity
15 are codified in publicly available computer programs. Preferred computer program methods to determine identity and similarity between two sequences include, but are not limited to, the GCG program package (Devereux, J., et al., *Nucleic Acids Research* 12(1): 387 (1984)), BLASTP, BLASTN, and FASTA (Atschul, S.F. et al., *J. Molec. Biol.* 215: 403-410 (1990)). The BLAST X program is publicly available from NCBI and other sources (*BLAST*
20 *Manual*, Altschul, S., et al., NCBI NLM NIH Bethesda, MD 20894; Altschul, S., et al., *J. Mol. Biol.* 215: 403-410 (1990)).

As an illustration, by a polynucleotide having a nucleotide sequence having at least, for example, 95% "identity" to a reference nucleotide sequence selected from the group consisting of the polynucleotide of the Sequence Listing is intended that the nucleotide
25 sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another
30 nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. These mutations of the reference sequence may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among

nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence.

Similarly, by a polypeptide having an amino acid sequence having at least, for example, 95% identity to a reference amino acid sequence of selected from the group consisting of the amino acids of the Sequence Listing is intended that the amino acid sequence of the polypeptide is identical to the reference sequence except that the polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the reference amino acid. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a reference amino acid sequence, up to 5% of the amino acid residues in the reference sequence may be deleted or substituted with another amino acid, or a number of amino acids up to 5% of the total amino acid residues in the reference sequence may be inserted into the reference sequence. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

The deposit referred to herein will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Micro-organisms for purposes of Patent Procedure. These deposits are provided merely as convenience to those of skill in the art and are not an admission that a deposit is required under 35 U.S.C. § 112. The sequence of the polynucleotides contained in the deposited material, as well as the amino acid sequence of the polypeptides encoded thereby, are incorporated herein by reference and are controlling in the event of any conflict with any description of sequences herein. A license may be required to make, use or sell the deposited material, and no such license is hereby granted.

The terms "fragment," "derivative" and "analogue" when referring to the polypeptide characterized by the deduced amino acid sequence herein, means a polypeptide which retains essentially the same biological function or activity as such polypeptide. Thus, an analogue includes a proprotein which can be activated by cleavage of the proprotein portion to produce an active mature polypeptide.

The polypeptide of the present invention may be a recombinant polypeptide, a natural polypeptide or a synthetic polypeptide, preferably a recombinant polypeptide.

The fragment, derivative or analogue of the polypeptide characterized by the deduced amino acid sequence herein may be (i) one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code, or (ii) one in which one or more of the amino acid residues includes a substituent group, or (iii) one in which the polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol), or (iv) one in which the additional amino acids are fused to the polypeptide, such as a leader or secretory sequence or a sequence which is employed for purification of the polypeptide or a proprotein sequence. Such fragments, derivatives and analogues are deemed to be within the scope of those skilled in the art from the teachings herein.

The polypeptides and polynucleotides of the present invention are preferably provided in an isolated form, and preferably are purified to homogeneity.

The term "isolated" means that the material is removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or polypeptide, separated from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotides could be part of a vector and/or such polynucleotides or polypeptides could be part of a composition, and still be isolated in that such vector or composition is not part of its natural environment.

The present invention also relates to vectors which include polynucleotides of the present invention, host cells which are genetically engineered with vectors of the invention and the production of polypeptides of the invention by recombinant techniques.

In accordance with yet a further aspect of the present invention, there is therefore provided a process for producing the polypeptide of the invention by recombinant techniques by expressing a polynucleotide encoding said polypeptide in a host and recovering the expressed product. Alternatively, the polypeptides of the invention can be synthetically produced by conventional peptide synthesizers.

Host cells are genetically engineered (transduced or transformed or transfected) with the vectors of this invention which may be, for example, a cloning vector or an expression vector. The vector may be, for example, in the form of a plasmid, a cosmid, a phage, etc. The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the

genes. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

5 Suitable expression vectors include chromosomal, nonchromosomal and synthetic DNA sequences, e.g., bacterial plasmids; phage DNA; baculovirus; yeast plasmids; vectors derived from combinations of plasmids and phage DNA. However, any other vector may be used as long as it is replicable and viable in the host.

10 The appropriate DNA sequence may be inserted into the vector by a variety of procedures. In general, the DNA sequence is inserted into an appropriate restriction endonuclease site(s) by procedures known in the art.

15 The DNA sequence in the expression vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct mRNA synthesis. As representative examples of such promoters, there may be mentioned: LTR or SV40 promoter, the *E. coli* *lac* or *trp*, the phage lambda P_L promoter and other promoters known to control expression of genes in eukaryotic or prokaryotic cells or their viruses. The expression vector also contains a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression.

20 In addition, the expression vectors preferably contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in *E. coli*.

25 The gene can be placed under the control of a promoter, ribosome binding site (for bacterial expression) and, optionally, an operator (collectively referred to herein as "control" elements), so that the DNA sequence encoding the desired protein is transcribed into RNA in the host cell transformed by a vector containing this expression construction. The coding sequence may or may not contain a signal peptide or leader sequence. The polypeptides of the present invention can be expressed using, for example, the *E. coli* *tac* promoter or the protein A gene (*spa*) promoter and signal sequence. Leader sequences can be removed by the bacterial host in post-translational processing. See, e.g., U.S. Patent Nos. 4,431,739; 30 4,425,437; 4,338,397. Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are PKK232-8 and PCM7. Particular named bacterial promoters include *lacI*, *lacZ*, T3, T7, *gpt*, lambda P_R, P_L and *trp*. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and

mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.

In addition to control sequences, it may be desirable to add regulatory sequences which allow for regulation of the expression of the protein sequences relative to the growth
5 of the host cell. Regulatory sequences are known to those of skill in the art, and examples include those which cause the expression of a gene to be turned on or off in response to a chemical or physical stimulus, including the presence of a regulatory compound. Other types of regulatory elements may also be present in the vector, for example, enhancer sequences.

10 An expression vector is constructed so that the particular coding sequence is located in the vector with the appropriate regulatory sequences, the positioning and orientation of the coding sequence with respect to the control sequences being such that the coding sequence is transcribed under the "control" of the control sequences (i.e., RNA polymerase which binds to the DNA molecule at the control sequences transcribes the coding
15 sequence). Modification of the coding sequences may be desirable to achieve this end. For example, in some cases it may be necessary to modify the sequence so that it may be attached to the control sequences with the appropriate orientation; i.e., to maintain the reading frame. The control sequences and other regulatory sequences may be ligated to the coding sequence prior to insertion into a vector, such as the cloning vectors described
20 above. Alternatively, the coding sequence can be cloned directly into an expression vector which already contains the control sequences and an appropriate restriction site.

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-
25 expressed gene to direct transcription of a downstream structural sequence. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal
30 identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product.

The vector containing the appropriate DNA sequence as hereinabove described, as well as an appropriate promoter or control sequence, may be employed to transform an appropriate host to permit the host to express the protein.

More particularly, the present invention also includes recombinant constructs comprising one or more of the sequences as broadly described above. The constructs comprise a vector, such as a plasmid or viral vector, into which a sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this
5 embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available. The following vectors are provided by way of example. Bacterial: pET-3 vectors (Stratagene), pQE70, pQE60, pQE-9 (Qiagen), pbs, pD10, phagescript, psiX174, pbluescript SK, pbsks,
10 pNH8A, pNH16a, pNH18A, pNH46A (Stratagene); ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pBlueBacIII (Invitrogen), pWLNEO, pSV2CAT, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia). However, any other plasmid or vector may be used as long as they are replicable and viable in the host.

15 Examples of recombinant DNA vectors for cloning and host cells which they can transform include the bacteriophage λ (*E. coli*), pBR322 (*E. coli*), pACYC177 (*E. coli*), pKT230 (gram-negative bacteria), pGV1106 (gram-negative bacteria), pLAFR1 (gram-negative bacteria), pME290 (non-*E. coli* gram-negative bacteria), pHV14 (*E. coli* and *Bacillus subtilis*), pBD9 (*Bacillus*), pIJ61 (*Streptomyces*), pUC6 (*Streptomyces*), YIp5
20 (*Saccharomyces*), a baculovirus insect cell system, YCp19 (*Saccharomyces*). See, generally, "DNA Cloning": Vols. I & II, Glover *et al.* ed. IRL Press Oxford (1985) (1987) and; T. Maniatis *et al.* ("Molecular Cloning" Cold Spring Harbor Laboratory (1982).

In some cases, it may be desirable to add sequences which cause the secretion of the polypeptide from the host organism, with subsequent cleavage of the secretory signal.

25 Polypeptides can be expressed in host cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, *et al.*, Molecular Cloning: A Laboratory Manual, Second Edition, Cold
30 Spring Harbor, N.Y., (1989), the disclosure of which is hereby incorporated by reference.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period.

Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use
5 of cell lysing agents, such methods are well known to those skilled in the art.

Depending on the expression system and host selected, the polypeptide of the present invention may be produced by growing host cells transformed by an expression vector described above under conditions whereby the polypeptide of interest is expressed. The polypeptide is then isolated from the host cells and purified. If the expression system
10 secretes the polypeptide into growth media, the polypeptide can be purified directly from the media. If the polypeptide is not secreted, it is isolated from cell lysates or recovered from the cell membrane fraction. Where the polypeptide is localized to the cell surface, whole cells or isolated membranes can be used as an assayable source of the desired gene product. Polypeptide expressed in bacterial hosts such as *E. coli* may require isolation from
15 inclusion bodies and refolding. Where the mature protein has a very hydrophobic region which leads to an insoluble product of overexpression, it may be desirable to express a truncated protein in which the hydrophobic region has been deleted. The selection of the appropriate growth conditions and recovery methods are within the skill of the art.

The polypeptide can be recovered and purified from recombinant cell cultures by
20 methods including ammonium sulphate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography
25 (HPLC) can be employed for final purification steps.

Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. Polypeptides of the invention may also include an initial methionine amino acid residue.

A "replicon" is any genetic element (e.g., plasmid, chromosome, virus) that
30 functions as an autonomous unit of DNA replication *in vivo*; i.e., capable of replication under its own control.

A "vector" is a replicon, such as a plasmid, phage, or cosmid, to which another DNA segment may be attached so as to bring about the replication of the attached segment.

A "double-stranded DNA molecule" refers to the polymeric form of deoxyribonucleotides (bases adenine, guanine, thymine, or cytosine) in a double-stranded helix, both relaxed and supercoiled. This term refers only to the primary and secondary structure of the molecule, and does not limit it to any particular tertiary forms. Thus, this term includes double-stranded DNA found, *inter alia*, in linear DNA molecules (e.g., restriction fragments), viruses, plasmids, and chromosomes. In discussing the structure of particular double-stranded DNA molecules, sequences may be described herein according to the normal convention of giving only the sequence in the 5' to 3' direction along the nontranscribed strand of DNA (i.e., the strand having the sequence homologous to the mRNA).

A DNA "coding sequence of" or a "nucleotide sequence encoding" a particular protein, is a DNA sequence which is transcribed and translated into a polypeptide when placed under the control of appropriate regulatory sequences.

A "promoter sequence" is a DNA regulatory region capable of binding RNA polymerase in a cell and initiating transcription of a downstream (3' direction) coding sequence. For purposes of defining the present invention, the promoter sequence is bound at the 3' terminus by a translation start codon (e.g., ATG) of a coding sequence and extends upstream (5' direction) to include the minimum number of bases or elements necessary to initiate transcription at levels detectable above background. Within the promoter sequence will be found a transcription initiation site (conveniently defined by mapping with nuclease S1), as well as protein binding domains (consensus sequences) responsible for the binding of RNA polymerase. Eukaryotic promoters will often, but not always, contain "TATA" boxes and "CAT" boxes. Prokaryotic promoters contain Shine-Dalgarno sequences in addition to the -10 and -35 consensus sequences.

DNA "control sequences" refers collectively to promoter sequences, ribosome binding sites, polyadenylation signals, transcription termination sequences, upstream regulatory domains, enhancers, and the like, which collectively provide for the expression (i.e., the transcription and translation) of a coding sequence in a host cell.

A control sequence "directs the expression" of a coding sequence in a cell when RNA polymerase will bind the promoter sequence and transcribe the coding sequence into mRNA, which is then translated into the polypeptide encoded by the coding sequence.

A "host cell" is a cell which has been transformed or transfected, or is capable of transformation or transfection by an exogenous DNA sequence.

A cell has been "transformed" by exogenous DNA when such exogenous DNA has been introduced inside the cell membrane. Exogenous DNA may or may not be integrated (covalently linked) into chromosomal DNA making up the genome of the cell. In prokaryotes and yeasts, for example, the exogenous DNA may be maintained on an episomal element, such as a plasmid. With respect to eukaryotic cells, a stably transformed or transfected cell is one in which the exogenous DNA has become integrated into the chromosome so that it is inherited by daughter cells through chromosome replication. This stability is demonstrated by the ability of the eukaryotic cell to establish cell lines or clones comprised of a population of daughter cell containing the exogenous DNA.

A "clone" is a population of cells derived from a single cell or common ancestor by mitosis. A "cell line" is a clone of a primary cell that is capable of stable growth *in vitro* for many generations.

A "heterologous" region of a DNA construct is an identifiable segment of DNA within or attached to another DNA molecule that is not found in association with the other molecule in nature.

This invention is also related to the use of the polynucleotides of the invention for use as diagnostic reagents. Detection of a polynucleotide or polypeptide of the invention in a eukaryote, particularly a mammal, and especially a human, will provide a diagnostic method for diagnosis of a disease. Eukaryotes (herein also "individual(s)"), particularly mammals, and especially humans, infected with an organism comprising a polynucleotide of the invention may be detected at the nucleic acid level by a variety of techniques.

Nucleic acids for diagnosis may be obtained from an infected individual's cells and tissues, such as bone, blood, muscle, cartilage, and skin. Genomic DNA may be used directly for detection or may be amplified enzymatically by using PCR or other amplification technique prior to analysis. RNA or cDNA may also be used in the same ways. Using amplification, characterization of the species and strain of prokaryote present in an individual, may be made by an analysis of the genotype of the prokaryote gene. Deletions and insertions can be detected by a change in size of the amplified product in comparison to the genotype of a reference sequence. Point mutations can be identified by hybridizing amplified DNA to labeled polynucleotide sequences of the invention. Perfectly matched sequences can be distinguished from mismatched duplexes by RNase digestion or by differences in melting temperatures. DNA sequence differences may also be detected by alterations in the electrophoretic mobility of the DNA fragments in gels, with or without denaturing agents, or by direct DNA sequencing. See, *e.g.*, Myers et al., *Science*, 230: 1242 (1985). Sequence changes at specific locations also may be

revealed by nuclease protection assays, such as RNase and S1 protection or a chemical cleavage method. See, e.g., Cotton et al., *Proc. Natl. Acad. Sci., USA*, 85: 4397-4401 (1985).

5 Cells carrying mutations or polymorphisms in the gene of the invention may also be detected at the DNA level by a variety of techniques, to allow for serotyping, for example. For example, RT-PCR can be used to detect mutations. It is particularly preferred to used RT-PCR in conjunction with automated detection systems, such as, for example, GeneScan. RNA or cDNA may also be used for the same purpose, PCR or RT-PCR. As an example, PCR primers complementary to a nucleic acid encoding a polypeptide of the invention can be used to identify
10 and analyze mutations. These primers may be used for, among other things, amplifying DNA isolated from a sample derived from an individual. The primers may be used to amplify the gene isolated from an infected individual such that the gene may then be subject to various techniques for elucidation of the DNA sequence. In this way, mutations in the DNA sequence may be detected and used to diagnose infection and to serotype and/or classify the infectious agent.

15 The invention further provides a process for diagnosing, disease, preferably bacterial infections, more preferably infections by *Streptococcus pneumoniae*, comprising determining from a sample derived from an individual a increased level of expression of polynucleotide having a sequence set forth in the Sequence Listing or a sequence of the invention. Increased or decreased expression of a polynucleotide of the invention can be measured
20 using any one of the methods well known in the art for the quantitation of polynucleotides, such as, for example, amplification, PCR, RT-PCR, RNase protection, Northern blotting and other hybridization methods.

In addition, a diagnostic assay in accordance with the invention for detecting over-expression of a polypeptide of the invention compared to normal control tissue samples may be
25 used to detect the presence of an infection, for example. Assay techniques that can be used to determine levels of a polypeptide of the invention, in a sample derived from a host are well-known to those of skill in the art. Such assay methods include radioimmunoassays, competitive-binding assays, Western Blot analysis and ELISA assays.

In accordance with yet a further aspect of the present invention, there is provided
30 the use of a polypeptide of the invention for therapeutic or prophylactic purposes, for example, as an antibacterial agent or a vaccine.

In accordance with another aspect of the present invention, there is provided the use of a polynucleotide of the invention for therapeutic or prophylactic purposes, in particular genetic immunisation.

In accordance with yet another aspect of the present invention, there are provided inhibitors to such polypeptides, useful as antibacterial agents. In particular, there are provided antibodies against such polypeptides.

Polypeptides of the invention may also be used to assess the binding of small molecule
5 substrates and ligands in, for example, cells, cell-free preparations, chemical libraries, and natural product mixtures. These substrates and ligands may be natural substrates and ligands or may be structural or functional mimetics. See, *e.g.*, Coligan *et al.*, *Current Protocols in Immunology* 1(2): Chapter 5 (1991).

The invention also provides a method of screening compounds to identify those which
10 enhance (agonist) or block (antagonist) the action of polypeptides or polynucleotides of the invention, particularly those compounds that are bacteriostatic and/or bacteriocidal. The method of screening may involve high-throughput techniques. For example, to screen for agonists or antagonists, a synthetic reaction mix, a cellular compartment, such as a membrane, cell envelope or cell wall, or a preparation of any thereof, comprising a polypeptide of the invention and a
15 labeled substrate or ligand of such polypeptide is incubated in the absence or the presence of a candidate molecule that may be an agonist or antagonist of a polypeptide of the invention. The ability of the candidate molecule to agonize or antagonize a polypeptide of the invention is reflected in decreased binding of the labeled ligand or decreased production of product from such substrate. Molecules that bind gratuitously, *i.e.*, without inducing the effects of a polypeptide of
20 the invention are most likely to be good antagonists. Molecules that bind well and increase the rate of product production from substrate are agonists. Detection of the rate or level of production of product from substrate may be enhanced by using a reporter system. Reporter systems that may be useful in this regard include but are not limited to colorimetric labeled substrate converted into product, a reporter gene that is responsive to changes in polynucleotide or
25 polypeptide activity, and binding assays known in the art.

Another example of an assay for antagonists of a polypeptide of the invention is a competitive assay that combines such polypeptide and a potential antagonist with polypeptide-binding molecules, recombinant polypeptide-binding molecules, natural substrates or ligands, or substrate or ligand mimetics, under appropriate conditions for a competitive inhibition assay.
30 Polypeptides of the invention can be labeled, such as by radioactivity or a colorimetric compound, such that the number of such polypeptide molecules bound to a binding molecule or converted to product can be determined accurately to assess the effectiveness of the potential antagonist.

Potential antagonists include small organic molecules, peptides, polypeptides and antibodies that bind to a polynucleotide or polypeptide of the invention and thereby inhibit or extinguish its activity. Potential antagonists also may be small organic molecules, a peptide, a polypeptide such as a closely related protein or antibody that binds the same sites on a binding molecule, without inducing an activities of a polypeptide of the invention, thereby preventing the action of such polypeptide by excluding it from binding.

Potential antagonists include a small molecule that binds to and occupies the binding site of the polypeptide thereby preventing binding to cellular binding molecules, such that normal biological activity is prevented. Examples of small molecules include but are not limited to small organic molecules, peptides or peptide-like molecules. Other potential antagonists include antisense molecules (see Okano, *J. Neurochem.* 56: 560 (1991); *OLIGODEOXYNUCLEOTIDES AS ANTISENSE INHIBITORS OF GENE EXPRESSION*, CRC Press, Boca Raton, FL (1988), for a description of these molecules). Preferred potential antagonists include compounds related to and variants of the polypeptides of the invention.

Each of the DNA sequences provided herein may be used in the discovery and development of antibacterial compounds. The encoded protein, upon expression, can be used as a target for the screening of antibacterial drugs. Additionally, the DNA sequences encoding the amino terminal regions of the encoded protein or Shine-Delgarno or other translation facilitating sequences of the respective mRNA can be used to construct antisense sequences to control the expression of the coding sequence of interest.

The invention also provides the use of the polypeptide, polynucleotide or inhibitor of the invention to interfere with the initial physical interaction between a pathogen and mammalian host responsible for sequelae of infection. In particular the molecules of the invention may be used: in the prevention of adhesion of bacteria, in particular gram positive bacteria, to mammalian extracellular matrix proteins on in-dwelling devices or to extracellular matrix proteins in wounds; to block protein-mediated mammalian cell invasion by, for example, initiating phosphorylation of mammalian tyrosine kinases (Rosenshine *et al.*, *Infect. Immun.* 60:2211 (1992); to block bacterial adhesion between mammalian extracellular matrix proteins and bacterial proteins that mediate tissue damage and; to block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques.

The antagonists and agonists of the invention may be employed, for instance, to inhibit and treat otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural

empyema and endocarditis, and most particularly meningitis, such as for example infection of cerebrospinal fluid.

Another aspect of the invention is a pharmaceutical composition comprising the above polypeptide, polynucleotide or inhibitor of the invention and a pharmaceutically acceptable carrier.

In a particular aspect the invention provides the use of an inhibitor of the invention as an antibacterial agent.

The invention further relates to the manufacture of a medicament for such uses.

The polypeptide may be used as an antigen for vaccination of a host to produce specific antibodies which have anti-bacterial action. This invention also contemplates the use of the DNA encoding the antigen as a component in a DNA vaccine as discussed more fully below.

The polypeptides or cells expressing them can be used as an immunogen to produce antibodies thereto. These antibodies can be, for example, polyclonal or monoclonal antibodies. The term antibodies also includes chimeric, single chain, and humanized antibodies, as well as Fab fragments, or the product of an Fab expression library. Various procedures known in the art may be used for the production of such antibodies and fragments.

Antibodies generated against the polypeptides of the present invention can be obtained by direct injection of the polypeptides into an animal or by administering the polypeptides to an animal, preferably a nonhuman. The antibody so obtained will then bind the polypeptides itself. In this manner, even a sequence encoding only a fragment of the polypeptides can be used to generate antibodies binding the whole native polypeptides. Such antibodies can then be used to isolate the polypeptide from tissue expressing that polypeptide.

Polypeptide derivatives include antigenically or immunologically equivalent derivatives which form a particular aspect of this invention.

The term 'antigenically equivalent derivative' as used herein encompasses a polypeptide or its equivalent which will be specifically recognised by certain antibodies which, when raised to the protein or polypeptide according to the present invention, interfere with the interaction between pathogen and mammalian host.

The term 'immunologically equivalent derivative' as used herein encompasses a peptide or its equivalent which when used in a suitable formulation to raise antibodies in a

vertebrate, the antibodies act to interfere with the interaction between pathogen and mammalian host.

In particular derivatives which are slightly longer or slightly shorter than the native protein or polypeptide fragment of the present invention may be used. In addition,
5 polypeptides in which one or more of the amino acid residues are modified may be used. Such peptides may, for example, be prepared by substitution, addition, or rearrangement of amino acids or by chemical modification thereof. All such substitutions and modifications are generally well known to those skilled in the art of peptide chemistry.

The polypeptide, such as an antigenically or immunologically equivalent derivative
10 or a fusion protein thereof is used as an antigen to immunize a mouse or other animal such as a rat or chicken. The fusion protein may provide stability to the polypeptide. The antigen may be associated, for example by conjugation, with an immunogenic carrier protein for example bovine serum albumin (BSA) or keyhole limpet haemocyanin (KLH). Alternatively a multiple antigenic peptide comprising multiple copies of the protein or
15 polypeptide, or an antigenically or immunologically equivalent polypeptide thereof may be sufficiently antigenic to improve immunogenicity so as to obviate the use of a carrier.

For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique (Kohler and Milstein, Nature, 256:495-497(1975)), the trioma technique, the
20 human B-cell hybridoma technique (Kozbor et al., Immunology Today 4:72(1983)), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole, et al., 1985, in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc., pp. 77-96).

Techniques described for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce single chain antibodies to immunogenic polypeptide
25 products of this invention.

Using the procedure of Kohler and Milstein (supra, (1975)), antibody-containing cells from the immunised mammal are fused with myeloma cells to create hybridoma cells secreting monoclonal antibodies.

The hybridomas are screened to select a cell line with high binding affinity and
30 favorable cross reaction with other Streptococcal species using one or more of the original polypeptide and/or the fusion protein. The selected cell line is cultured to obtain the desired Mab.

Hybridoma cell lines secreting the monoclonal antibody are another aspect of this invention.

Alternatively phage display technology could be utilised to select antibody genes with binding activities towards the polypeptide either from repertoires of PCR amplified v-genes of lymphocytes from humans screened for possessing anti-Fbp or from naive libraries (McCafferty, J. *et al.*, Nature 348:552-554(1990), and Marks, J. *et al.*, Biotechnology 10:779-783(1992)). The affinity of these antibodies can also be improved by chain shuffling (Clackson, T. *et al.*, Nature 352:624-628(1991)).

The antibody should be screened again for high affinity to the polypeptide and/or fusion protein.

As mentioned above, a fragment of the final antibody may be prepared.

The antibody may be either intact antibody of M_r approx 150,000 or a derivative of it, for example a Fab fragment or a Fv fragment as described in Skerra, A and Pluckthun, A., Science 240:1038-1040 (1988). If two antigen binding domains are present each domain may be directed against a different epitope - termed 'bispecific' antibodies.

The antibody of the invention may be prepared by conventional means for example by established monoclonal antibody technology (Kohler, G. and Milstein, C. (*supra*, (1975) or using recombinant means e.g. combinatorial libraries, for example as described in Huse, W.D. *et al.*, Science 246:1275-1281 (1989).

Preferably the antibody is prepared by expression of a DNA polymer encoding said antibody in an appropriate expression system such as described above for the expression of polypeptides of the invention. The choice of vector for the expression system will be determined in part by the host, which may be a prokaryotic cell, such as *E. coli* (preferably strain B) or *Streptomyces sp.* or a eukaryotic cell, such as a mouse C127, mouse myeloma, human HeLa, Chinese hamster ovary, filamentous or unicellular fungi or insect cell. The host may also be a transgenic animal or a transgenic plant (for example, as described in Hiatt, A. *et al.*, Nature 340:76-78(1989). Suitable vectors include plasmids, bacteriophages, cosmids and recombinant viruses, derived from, for example, baculoviruses and vaccinia.

The Fab fragment may also be prepared from its parent monoclonal antibody by enzyme treatment, for example using papain to cleave the Fab portion from the Fc portion.

Preferably the antibody or derivative thereof is modified to make it less immunogenic in the patient. For example, if the patient is human the antibody may most preferably be 'humanised'; where the complementarity determining region(s) of the hybridoma-derived antibody has been transplanted into a human monoclonal antibody, for example as described in Jones, P. *et al.*, Nature 321:522-525 (1986), or Tempest *et al.*, Biotechnology 9:266-273 (1991).

The modification need not be restricted to one of 'humanisation' ; other primate sequences (for example Newman, R. *et al.*, Biotechnology 10:1455-1460 (1992)) may also be used.

5 The humanised monoclonal antibody, or its fragment having binding activity, form a particular aspect of this invention.

This invention provides a method of screening drugs to identify those which interfere with the proteins selected as targets herein, which method comprises measuring the interference of the activity of the protein by a test drug. For example if the protein selected has a catalytic activity, after suitable purification and formulation the activity of the enzyme
10 can be followed by its ability to convert its natural substrates. By incorporating different chemically synthesised test compounds or natural products into such an assay of enzymatic activity one is able to detect those additives which compete with the natural substrate or otherwise inhibit enzymatic activity.

The invention also relates to inhibitors identified thereby.

15 The use of a polynucleotide of the invention in genetic immunisation will preferably employ a suitable delivery method such as direct injection of plasmid DNA into muscles (Wolff *et al.*, Hum. Mol. Genet. 1:363 (1992); Manthorpe *et al.*, Hum. Gene Ther. 4:419 (1993)), delivery of DNA complexed with specific protein carriers (Wu *et al.*, J. Biol. Chem. 264:16985 (1989)), coprecipitation of DNA with calcium phosphate
20 (Benvenisty & Reshef, Proc. Nat'l Acad. Sci. USA, 83:9551 (1986)), encapsulation of DNA in various forms of liposomes (Kaneda *et al.*, Science 243:375 (1989)), particle bombardment (Tang *et al.*, Nature 356:152 (1992)); Eisenbraun *et al.*, DNA Cell Biol. 12:791 (1993)) and *in vivo* infection using cloned retroviral vectors (Seeger *et al.*, Proc. Nat'l Acad. Sci. USA 81:5849 (1984)). Suitable promoters for muscle transfection include
25 CMV, RSV, SRa, actin, MCK, alpha globin, adenovirus and dihydrofolate reductase.

In therapy or as a prophylactic, the active agent i.e., the polypeptide, polynucleotide or inhibitor of the invention, may be administered to a patient as an injectable composition, for example as a sterile aqueous dispersion, preferably isotonic.

Alternatively the composition may be formulated for topical application
30 for example in the form of ointments, creams, lotions, eye ointments, eye drops, ear drops, mouthwash, impregnated dressings and sutures and aerosols, and may contain appropriate conventional additives, including, for example, preservatives, solvents to assist drug penetration, and emollients in ointments and creams. Such topical formulations may also contain compatible conventional carriers, for example cream or ointment bases, and ethanol

or oleyl alcohol for lotions. Such carriers may constitute from about 1% to about 98% by weight of the formulation; more usually they will constitute up to about 80% by weight of the formulation.

5 For administration to human patients, it is expected that the daily dosage level of the active agent will be from 0.01 to 10 mg/kg, typically around 1 mg/kg. The physician in any event will determine the actual dosage which will be most suitable for an individual patient and will vary with the age, weight and response of the particular patient. The above dosages are exemplary of the average case. There can, of course, be individual instances where higher or lower dosage ranges are merited, and such are within the scope of this
10 invention.

A vaccine composition is conveniently in injectable form. Conventional adjuvants may be employed to enhance the immune response.

A suitable unit dose for vaccination is 0.5-5 µg/kg of antigen, and such dose is preferably administered 1-3 times and with an interval of 1-3 weeks.

15 Within the indicated dosage range, no adverse toxicological effects are expected with the compounds of the invention which would preclude their administration to suitable patients.

In order to facilitate understanding of the following example certain frequently occurring methods and/or terms will be described.

20 "Plasmids" are designated by a lower case p preceded and/or followed by capital letters and/or numbers. The starting plasmids herein are either commercially available, publicly available on an unrestricted basis, or can be constructed from available plasmids in accord with published procedures. In addition, equivalent plasmids to those described are known in the art and will be apparent to the ordinarily skilled artisan.

25 "Digestion" of DNA refers to catalytic cleavage of the DNA with a restriction enzyme that acts only at certain sequences in the DNA. The various restriction enzymes used herein are commercially available and their reaction conditions, cofactors and other requirements were used as would be known to the ordinarily skilled artisan. For analytical purposes, typically 1 µg of plasmid or DNA fragment is used with about 2 units of enzyme
30 in about 20 µl of buffer solution. For the purpose of isolating DNA fragments for plasmid construction, typically 5 to 50 µg of DNA are digested with 20 to 250 units of enzyme in a larger volume. Appropriate buffers and substrate amounts for particular restriction enzymes are specified by the manufacturer. Incubation times of about 1 hour at 37° C are ordinarily

used, but may vary in accordance with the supplier's instructions. After digestion the reaction is electrophoresed directly on a polyacrylamide gel to isolate the desired fragment.

Size separation of the cleaved fragments is performed using 8 percent polyacrylamide gel described by Goeddel, D. *et al.*, (1980) *Nucleic Acids Res.*, 8:4057.

5 "Oligonucleotides" refers to either a single stranded polydeoxynucleotide or two complementary polydeoxynucleotide strands which may be chemically synthesized. Such synthetic oligonucleotides have no 5' phosphate and thus will not ligate to another oligonucleotide without adding a phosphate with an ATP in the presence of a kinase. A synthetic oligonucleotide will ligate to a fragment that has not been dephosphorylated.

10 "Ligation" refers to the process of forming phosphodiester bonds between two double stranded nucleic acid fragments (Maniatis, T., *et al.*, supra, p. 146). Unless otherwise provided, ligation may be accomplished using known buffers and conditions with 10 units to T4 DNA ligase ("ligase") per 0.5 µg of approximately equimolar amounts of the DNA fragments to be ligated.

15 **Example 1**

Isolation of DNA coding for a virulence gene in *Streptococcus pneumoniae*

As mentioned above each of the DNAs disclosed herein by virtue of the fact that it includes an intact open reading frame is useful to a greater or lesser extent as a screen for identifying antimicrobial compounds. A useful approach for selecting the preferred DNA
20 sequences for screen development is evaluation by insertion-duplication mutagenesis. This system disclosed by Morrison *et al.*, J. Bacteriol. 159:870 (1984), is applied as follows.

Briefly, random fragments of *Streptococcus pneumoniae*, strain 0100993 DNA are generated enzymatically (by restriction endonuclease digestion) or physically (by sonication based shearing) followed by gel fractionation and end repair employing T4 DNA
25 polymerase. It is preferred that the DNA fragments so produced are in the range of 200-400 base pairs, a size sufficient to ensure homologous recombination and to insure a representative library in *E.coli*. The fragments are then inserted into appropriately tagged plasmids as described in Hensel *et al.*, Science 269: 400-403(1995). Although a number of plasmids can be used for this purpose, a particularly useful plasmid is pJDC9 described by
30 Pearce *et al.*, Mol. Microbiol. 9:1037 (1993) which carries the *erm* gene facilitating erythromycin selection in either *E. coli* or *S. pneumoniae* previously modified by incorporation of DNA sequence tags into one of the polylinker cloning sites. The tagged plasmids are introduced into the appropriate *S. pneumoniae* strain selected, *inter alia*, on the basis of serotype and virulence in a murine model of pneumococcal pneumonia.

It is appreciated that a seventeen amino acid competence factor exists (Havastein et al., Proc. Nat'l. Acad. Sci. USA 92:11140-44 (1995)) and may be usefully employed in this protocol to increase the transformation frequencies. A proportion of transformants are analysed to verify homologous integration and as a check on stability. Unwanted levels of reversion are minimized because the duplicated regions will be short (200-400 bp), however if significant reversion rates are encountered they may be modulated by maintaining antibiotic selection during the growth of the transformants in culture and/or during growth in the animal.

The *S. pneumoniae* transformants are pooled for inoculation into mice, eg., Swiss and/or C57B1/6. Preliminary experiments are conducted to establish the optimum complexity of the pools and level of inoculum. A particularly useful model has been described by Veber et al. (J. Antimicrobiol. Chemother. 32:432 (1993) in which 10^5 cfu inocula sizes are introduced by mouth to the trachea. Strain differences are observed with respect to onset of disease e.g., 3-4 days for Swiss mice and 8-10 days for C57B1/6. Infection yields in the lungs approach 10^8 cfu/lung. IP administration is also possible when genes mediating blood stream infection are evaluated. Following optimization of parameters of the infection model, the mutant bank normally comprising several thousand strains is subjected to the virulence test. Mutants with attenuated virulence are identified by hybridization analysis using the labelled tags from the "input" and "recovered" pools as probes as described in Hensel et al., Science 269: 400-403(1995). *S. pneumoniae* DNA is colony blotted or dot blotted, DNA flanking the integrated plasmid is cloned by plasmid rescue in *E. coli* (Morrison et al., J. Bacteriol. 159:870 (1984)) and sequenced. Following sequencing, the DNA is compared to the nucleotide sequences given herein and the appropriate ORF is identified and function confirmed for example by knock-out studies. Expression vectors providing the selected protein are prepared and the protein is configured in an appropriate screen for the identification of anti-microbial agents. Alternatively, genomic DNA libraries are probed with restriction fragments flanking the integrated plasmid to isolate full-length cloned virulence genes whose function can be confirmed by "knock-out" studies or other methods, which are then expressed and incorporated into a screen as described above.

The individual full length sequences given herein are summarized in the following Tables (Table 1 and Table 2). Under the column in Table 1 labeled "Identity" there is the deduced identity of each open reading frame of the invention determined using Blastp and/or MPSearch. The ORF# column indicates whether the polynucleotide encoding each

ORF encodes more than one ORF. For example, SEQ ID NO:224 has an ORF# 1 but no #2; thus the polynucleotide encodes this ORF#1, but no other ORF was detected. On the other hand, SEQ ID NO:225 and 226 have ORF#s 1 and 2 respectively, indicating that they were both encoded by the same polynucleotide. This can also be seen in Table 2 where the polynucleotide of SEQ ID NO: 2 encodes the ORFs of SEQ ID NOS: 225 and 226. Table 1 also shows the start ("START" column) and stop ("STOP" column) codons for each ORF and their positions in the encoding polynucleotide sequence. The SEQ ID NOS of the polypeptides of this table are linked to both a deduced identity in this table and a polynucleotide sequence in Table 2 which encodes each polypeptide. The "Direction" column in Table 1 shows the direction of the ORF encoding each polypeptide in this table. "Forward" denotes the sense orientation and "Reverse" denotes the antisense orientation of the ORF.

TABLE 1

SEQ ID NO:	Identity	ORF #	Codon		Position		Direction
			Start	Stop	Start	Stop	
224.	Phosphate Transport ATP-Binding Protein PSTB. - <i>Escherichia</i>	1	-CAT	TCA-	2	553	Reverse
225.	probable ATP binding protein - <i>Bacillus subtilis</i>	1	-CAT	TCA-	38	781	Reverse
226.	Nopaline Transport System Permease Protein Nocr. - <i>Agrobacterium Tumefaciens</i>	2	-CAG	TTA-	781	1512	Reverse
227.	Aspartate Aminotransferase A (EC 2.6.11) (Transaminase A) (ASPAT.) - <i>Rhizobium Meliloti</i> .	1	ATG	TAG	480	671	Forward
228.	ISL2 protein - <i>Lactobacillus helveticus</i>	1	ATG	TAA	549	947	Forward
229.	ISL2 protein - <i>Lactobacillus helveticus</i>	2	ATG	TAG	889	1353	Forward
230.	Unknown	3	ATG	TGA	1421	1570	Forward
231.	Unknown	2	-CAT	CTA-	111	413	Reverse
232.	Unknown	1	ATG	TGA	133	282	Forward
233.	Acyl Carrier Protein (ACP.) - <i>Rhizobium Meliloti</i> .	1	-CAT	CTA-	673	906	Reverse
234.	Unknown	1	-CAT	TTA-	15	137	Reverse
235.	Unknown	2	-CAT	CTA-	681	989	Reverse
236.	Sulfate Transport System Permease Protein CYST (Fragment). - <i>Synechocystis SP.</i> (Strain PCC 6803).	2	-CAT	TTA-	336	689	Reverse
237.	probable transposase (insertion sequence IS861) - <i>Streptococcus agalactiae</i> (strain COH-1)	2	-CAT	TCA-	149	454	Reverse
238.	Unknown	2	-CAG	TTA-	567	851	Reverse
239.	"PTS SYSTEM	1	ATG	TAA	49	477	Forward
240.	"PTS SYSTEM	2	-CAT	TTA-	151	789	Reverse
241.	nitrogen fixation protein (nifS) homolog - <i>Haemophilus influenzae</i> (strain Rd KW 20)	1	-CAT	TCA-	1	207	Reverse
242.	cellobiose phosphotransferase system celA - <i>Bacillus stearothermophilus</i>	1	-CAT	TCA-	84	431	Reverse
243.	surface protein PspA - <i>Streptococcus pneumoniae</i>	1	ATG	TAA	22	321	Forward
244.	Unknown	2	ATG	TAA	272	469	Forward
245.	ATP-dependent Clp proteinase (EC 3.4.21.-) chain clpL - <i>Lactococcus lactis</i> subs p. lactis	1	ATG	TGA	83	760	Forward

	plasmid pUCL22						
246.	Beta-Glucosidase (EC3.2.1.21) (Gentiobiase) (Cellobiase)) (Beta-D- Glucoside GL Ucohydrolase) (Amygdalase). - Bacillus Subtilis.	1	-CAT	TCA-	153	599	Reverse
247.	Glycine Betaine/L-Proline Transport ATP - Binding Protein Prov. - Escherichia Col. I.	2	ATG	TAA	159	887	Forward
248.	Unknown	3	-CAT	TTA-	1102	1254	Reverse
249.	30S Ribosomal Protein S11 (BS11). - Bacillus Subtilis.	1	ATG	TGA	15	164	Forward
250.	DNA - Directed RNA Polymerase Alpha Chain (EC 2.7.7.6) (Transcriptase Alpha Chain). - Bacillus Subtilis.	2	ATG	TAA	282	1217	Forward
251.	Peptide Chain Release Factor 3 (RF-3). - Bacteroides Nodosus (Dichelobacter Nod Osus).	1	ATG	TAG	212	667	Forward
252.	Unknown	1	ATG	TAG	267	353	Forward
253.	Riboflavin Synthase Alpha Chain (EC 2.5.1.9). - Bacillus Subtilis.	2	-CAT	CTA-	213	662	Reverse
254.	Unknown	3	-CAT	TTA-	833	1045	Reverse
255.	Unknown	1	-CAT	TTA-	83	424	Reverse
256.	mesI protein - Leuconostoc mesenteroides	2	ATG	TAG	448	1302	Forward
257.	Transacetylase BMTD (EC 2.3.1.-). - Bacillus Subtilis.	1	CTG	TAG	3	320	Forward

SEQ ID NO:	Identity	ORF #	Codon		Position		Direction
			Start	Stop	Start	Stop	
258.	ribose-phosphate pyrophosphokinase (EC 2.7.6.1.) - <i>Bacillus caldolyticus</i>	1	CTG	TAG	1	642	Forward
259.	Unknown	1	ATG	TAA	66	614	Forward
260.	Unknown	1	ATG	TAG	108	590	Forward
261.	nitrogenase C (nifC) homolog - <i>Haemophilus influenzae</i> (strain Rd KW20)	2	ATG	TAG	631	855	Forward
262.	Unknown	2	ATG	TAA	606	752	Forward
263.	Unknown	2	ATG	TGA	280	495	Forward
264.	Unknown	2	ATG	TGA	639	1466	Forward
265.	Acetyl Esterase (EC 3.1.-.-) - <i>Caldocellum Saccharolyticum</i> .	2	ATG	TAA	274	594	Forward
266.	Unknown	1	-CAT	TCA-	2	157	Reverse
267.	Triosephosphate Isomerase (EC 5.3.1.1) (TIM). - <i>Bacillus Subtilis</i> .	1	-CAT	TTA-	270	665	Reverse
268.	Branched-chain Amino Acid Aminotransferase (EC 2.6.1.42) (Transaminase B). - <i>ES Cherichia Coli</i> .	1	ATG	TAG	110	736	Forward
269.	branched-chain-amino-acid transaminase homolog - <i>Haemophilus influenzae</i> (strain Rd KW20)	2	ATG	TAA	708	842	Forward
270.	DnaK protein - <i>Lactococcus lactis</i>	1	CTG	TGA	3	749	Forward
271.	Ketol-Acid Reductoisomerase (EC 1.1.1.86) (Acetohydroxy-Acid Isomeroreductase). - <i>Lactococcus Lactis</i> (Subsp. Lactis) (<i>Streptococcus Lactis</i>)	1	ATG	TAA	99	428	Forward
272.	Unknown	1	-CAT	CTA-	278	631	Reverse
273.	Amidophosphoribosyltransferase Precursor (EC 2.4.2.14) (Glutamine Phosphoribosylpyrophosphate Amidotransferase) (Atase). - <i>Bacillus Subtilis</i> .	2	-CAT	CTA-	152	775	Reverse
274.	Proline-Carboxylate Peptidase (EC 3.4.19.3) (5-Oxoprolyl-Peptidase). - <i>STR Eptococcus Pvoenes</i> .	1	-CAT	TCA-	156	803	Reverse
275.	50S Ribosomal Protein L16. - <i>Mycoplasma Capricolum</i> .	1	ATG	TAA	33	416	Forward
276.	serine O-acetyltransferase (EC 2.3.1.30) - <i>Bacillus stearothermophilus</i>	2	-CAT	CTA-	577	1194	Reverse
277.	Unknown	1	ATG	TAG	61	648	Forward

278.	Unknown	1	-CAT	CTA~	165	335	Reverse
279.	Lipoprotein Signal Peptidase (EC 3.4.23.36) (Prolipoprotein Signal Peptidase) (Signal Peptidase II) (Spase II). - <i>Staphylococcus Aureus</i> .	1	ATG	TAA	56	517	Forward
280.	Unknown	1	ATG	TAA	214	534	Forward
281.	Alpha-Acetolactate Decarboxylase (EC 4.1.1.5). - <i>Bacillus Subtilis</i> .	1	-CAT	CTA~	104	445	Reverse
282.	Dihydrodipicolinate Synthase 9EC 4.2.1.52) (DHDPS). - <i>Bacillus Subtilis</i> .	3	-CAT	TCA~	675	884	Reverse
283.	Polyribonucleotide Nucleotidyltransferase (EC 2.7.7.8) (Polynucleotide Phosphorylase) (Pnpase). - <i>Photobacterium Luminescens</i> .	1	-CAT	TCA~	1	855	Reverse
284.	Single-Strand Binding Protein (SSB) (Helix-Destabilizing Protein). - <i>Bacillus S Ubtilis</i>	1	-CAT	TTA~	128	598	Reverse
285.	ATP-Dependent CLP Protease ATO-Binding Subunit CLPX. - <i>Escherichia Coli</i> .	2	-CAT	CTA~	195	482	Reverse
286.	ATP-Dependent CLP Protease ATO-Binding Subunit CLPX. - <i>Escherichia Coli</i>	4	-CAG	TCA~	676	990	Reverse
287.	N-(5'-Phosphoribosyl) Anthranilate Isomerase (EC 5.3.1.24) (PRAI). - <i>Lactococcus Lactis</i> (Subsp. Lactis) (<i>Streptococcus Lactis</i>).	1	ATG	TAA	83	712	Forward
288.	30S Ribosomal Protein S2. - <i>Escherichia Coli</i> .	1	ATG	TGA	277	591	Forward
289.	30S Ribosomal Protein S2. - <i>Escherichia Coli</i> .	3	ATG	TGA	918	1064	Forward
290.	Possible beta-galactosidase precursor	1	-CAT	CTA~	120	545	Reverse
291.	Unknown	1	-CAT	TTA~	77	283	Reverse
292.	Unknown	1	-CAT	TTA~	1	198	Reverse
293.	"Phospho-2-Dehydro-3-Deoxyheptonate Aldolase	1	-CAT	TTA~	217	690	Reverse

SEQ ID NO:	Identity	ORF #	Codon		Position		Direction
			Start	Stop	Start	Stop	
294.	Unknown	2	-CAT	TTA-	429	599	Reverse
295.	Unknown	3	-CAT	TCA-	739	936	Reverse
296.	Sorbitol Dehydrogenase (EC 1.1.1.14) (L-Iditol 2-Dehydrogenase). - <i>Bacillus Subtilis</i> .	1	ATG	TAA	64	480	Forward
297.	EBG Operon Repressor. - <i>Escherichia Coli</i> .	2	-CAT	CTA-	668	1060	Reverse
298.	cellobiose phosphotransferase system celA - <i>Bacillus stearothermophilus</i>	2	-CAT	TTA-	249	566	Reverse
299.	Unknown	3	-CAT	TCA-	581	964	Reverse
300.	Adenylosuccinate Lyase (EC 4.3.2.2) (Adenylosuccinase) (ASL). - <i>Bacillus Subtilis</i> .	1	-CAT	TTA-	99	809	Reverse
301.	ATP-Binding Protein BEXA. - <i>Haemophilus Influenzae</i> .	1	ATG	TGA	111	404	Forward
302.	L-Lactate Dehydrogenase (Cytochrome) (EC 1.1.2.3). - <i>Escherichia Coli</i> .	2	ATG	TAA	337	507	Forward
303.	Phosphate Transport System Permease Protein PSTC. - <i>Escherichia Coli</i> .	3	ATG	TGA	507	1070	Forward
304.	Sulfate Transport ATP-Binding Protein Cysa. - <i>Synechococcus SP.</i> (Strain PCC 7942) (<i>Anacystis Nidulans</i> R2).	1	-CAT	CTA-	110	838	Reverse
305.	Unknown	2	-CAT	TTA-	838	1077	Reverse
306.	Unknown	2	-CAT	TCA-	282	749	Reverse
307.	Unknown	2	ATG	TAG	1108	1290	Forward
308.	Phosphoribosylformylglycinamide Cyclo-Ligase (EC 6.3.3.1) (AIRS) (Phosphoribosyl-Aminoimidazole Synthetase) (AIR Synthase). - <i>Bacillus Subtilis</i> .	2	-CAT	TCA-	331	477	Reverse
309.	Unknown	2	ATG	TAA	313	765	Forward
310.	SMS Protein. - <i>Escherichia Coli</i> .	1	-CAT	TCA-	102	416	Reverse
311.	sigma 42 protein - <i>Enterococcus faecalis</i>	1	-CAT	TCA-	8	487	Reverse
312.	Unknown	1	-CAT	TTA-	76	390	Reverse
313.	Guanylate Kinase (EC 2.7.4.8) (GMP Kinase). - <i>Escherichia Coli</i> .	2	-CAG	TTA-	415	849	Reverse
314.	Unknown	1	-CAT	TCA-	51	296	Reverse
315.	Unknown	1	ATG	TAA	175	285	Forward
316.	Unknown	2	ATG	TAA	361	558	Forward
317.	Unknown	3	ATG	TAA	383	1144	Forward

318.	"PTS System	2	-CAT	TCA~	166	465	Reverse
319.	L-Fucose Isomerase (EC 5.3.1.-) - Escherichia Coli.	1	-CAT	CTA~	9	482	Reverse
320.	Unknown	2	-CAT	TTA~	495	650	Reverse
321.	Unknown	1	ATG	TGA~	130	231	Forward
322.	3-Oxoacyl-[Acyl-Carrier Protein] Reductase (EC 1.1.1.100) (3-Ketoacyl- Acyl Car Rier Protein Reductase). - Escherichia Coli.	1	-CAT	TCA~	51	200	Reverse
323.	3-Oxoacyl-[Acyl-Carrier Protein] Reductase (EC 1.1.1.100) (3-Ketoacyl- Acyl Car Rier Protein Reductase). - Escherichia Coli.	2	-CAT	TCA~	231	614	Reverse
324.	2-Isopropylmalate Synthase (EC 4.1.3.12) (Alpha-Isopropylmalate Synthase) (Alph A- IPM Synthetase). - Lactococcus Lactis (Subsp. Lactis) (Streptococcus Lactis).	1	-CAT	TTA~	31	231	Reverse
325.	2-Isopropylmalate Synthase (EC 4.1.3.12) (Alpha-Isopropylmalate Synthase) (Alph A- IPM Synthetase). - Lactococcus Lactis (Subsp. Lactis) (Streptococcus Lactis).	2	-CAT	TCA~	191	334	Reverse
326.	Unknown	3	-CAT	TCA~	309	452	Reverse
327.	2-Isopropylmalate Synthase (EC 4.1.3.12) (Alpha-Isopropylmalate Synthase) (Alph A- IPM Synthetase). - Lactococcus Lactis (Subsp. Lactis) (Streptococcus Lactis).	4	-CAT	TTA~	495	1127	Reverse
328.	Unknown	2	-CAT	TCA~	170	469	Reverse
329.	Unknown	1	ATG	TAG	105	473	Forward
330.	Strscaa Ncbi gi: 310629NCBI gi: 473 - Streptococcus gordonii (strain PK488) DNA	1	-CAG	CTA~	81	665	Reverse

SEQ ID NO:	Identity	ORF #	Codon		Position		Direction
			Start	Stop	Start	Stop	
331.	Unknown	1	ATG	TGA	228	374	Forward
332.	lysyl aminopeptidase (EC 3.4.11.15) precursor - <i>Lactococcus lactis</i>	1	-CAT	TCA-	107	766	Reverse
333.	Indole-3-Glycerol Phosphate Synthase (EC 4.1.1.48) (IGPS). - <i>Lactococcus Lactis</i> (SUBSP. <i>Lactis</i>) (<i>Streptococcus Lactis</i>)	1	-CAT	TCA-	127	369	Reverse
334.	Anthranilate Phosphoribosyltransferase (EC 2.4.2.18).- <i>Lactococcus Lactis</i> (Sub SP. <i>Lactis</i>) (<i>Streptococcus Lactis</i>).	2	-CAA	TCA-	366	641	Reverse
335.	Tagatose-6-Phosphate Kinase (EC 2.7.1.-) (Phosphotagatokinase). - <i>Lactococcus L. Actis</i> (Subsp. <i>Lactis</i>) (<i>Streptococcus Lactis</i>)	1	ATG	TGA	42	524	Forward
336.	Unknown	1	ATG	TGA	73	474	Forward
337.	Unknown	1	-CAT	TTA-	32	286	Reverse
338.	Unknown	1	ATG	TGA	306	572	Forward
339.	Acetolactate Synthase Large Subunit (EC 4.1.3.18) (AHAS) (Acetphydroxy-Acid Synthase Large Subunit) (ALS). - <i>Lactococcus Lactis</i> (SUBSP. <i>Lactis</i>) (<i>Streptococcus Lactis</i>).	1	ATG	TAG	59	502	Forward
340.	Penicillin-Binding Proteins 1A/1B. - <i>Bacillus Subtilis</i> .	2	ATG	TGA	535	720	Forward
341.	Unknown	1	ATG	TAG	165	488	Forward
342.	Anthranilate Phosphoribosyltransferase (EC 2.4.2.18). - <i>Lactococcus Lactis</i> (SUB SP. <i>Lactis</i>) (<i>Streptococcus Lactis</i>).	1	-CAT	TCA-	5	394	Reverse
343.	grpE protein - <i>Lactococcus Lactis</i>	2	ATG	TAA	124	543	Forward
344.	Unknown	1	-CAT	CTA-	34	195	Reverse
345.	Unknown	2	-CAT	TTA-	377	544	Reverse
346.	Unknown	2	ATG	TAA	159	503	Forward
347.	Unknown	2	-CAT	CTA-	315	644	Reverse
348.	Unknown	2	-CAT	CTA-	468	587	Reverse
349.	Unknown	2	-CAT	CTA-	482	631	Reverse
350.	Unknown	2	-CAT	TTA-	380	757	Reverse
351.	NIFS Protein Homolog (Fragment). - <i>Lactobacillus Delbrueckii</i> (SUBSP. <i>Bulgaricus</i>).	1	ATG	TAG	87	797	Forward
352.	"Ornithine Carbamoyltransferase	1	TTG	TAA	2	502	Forward

353.	PSEGLI NCBI gi: 499660 - <i>Pseudomonas putida</i> .	1	-CAT	TTA~	50	481	Reverse
354.	Unknown	1	CTG	TAA	1	522	Forward
355.	Thioredoxin. - <i>Streptomyces Clavuligerus</i> .	1	ATG	TAG	58	375	Forward
356.	D-alanine permease (dagA) homolog - <i>Haemophilus influenzae</i> (strain Rd KW20)	1	ATG	TAG	185	343	Forward
357.	Unknown	1	-CAT	TTA~	78	371	Reverse
358.	"DNA Polymerase III	1	-CAA	TCA~	82	561	Reverse
359.	Transport ATP-Binding Protein Coma. - <i>Streptococcus Pneumoniae</i> .	1	-CAT	TTA~	112	552	Reverse
360.	Unknown	2	ATG	TAA	445	540	Forward
361.	surface protein PspA - <i>Streptococcus pneumoniae</i>	1	-CAT	TCA~	45	416	Reverse
362.	Licid Protein. - <i>Haemophilus Influenzae</i>	2	ATG	TAA	268	633	Forward
363.	Unknown	2	ATG	TAA	527	640	Forward
364.	Glutamine Transport ATP- Binding Protein GLNQ. - <i>Escherichia Coli</i> .	1	CTG	TGA	1	393	Forward
365.	Unknown	1	ATG	TAG	184	303	Forward
366.	Unknown	1	ATG	TGA	794	919	Forward
367.	Lipoamide Dehydrogenase Component (E3) of Pyruvate Dehydrogenase Complex (EC 1.8.1.4) (Dihydrolipoamide Dehydrogenase). - <i>Azotobacter Vinelandii</i> .	1	ATG	TAA	3	416	Forward

SEQ ID NO:	Identity	ORF #	Codon	Start	Stop	Position	Start	Stop	Direction
368.	Orotate Phosphoribosyltransferase (EC 2.4.2.10) (OPRT). - <i>Bacillus Subtilis</i> .	1	-CAT	CTA~		21		311	Reverse
369.	Unknown	1	ATG	TAA		28		309	Forward
370.	SPO0B-Associated GTP-Binding Protein. - <i>Bacillus Subtilis</i> .	1	ATG	TGA		110		538	Forward
371.	Transport ATP-Binding Protein COMA. - <i>Streptococcus Pneumoniae</i> .	1	-CAA	TCA~		47		679	Reverse
372.	prephenate dehydrogenase (EC 1.3.1.12) - <i>Lactococcus lactis</i> .	2	ATG	TAG		271		492	Forward
373.	O-Sialoglycoprotein Endopeptidase (EC 3.4.24.57) (Glycoprotease). - <i>Pasteurella Haemolytica</i> .	1	CTG	TAA		1		450	Forward
374.	Unknown	1	-CAT	TTA~		7		282	Reverse
375.	Unknown	1	TTG	TAA		2		265	Forward
376.	"DNA Polymerase III	1	ATG	TGA		3		401	Forward
377.	Unknown	2	ATG	TAA		361		516	Forward
378.	Dihydrodipicolinate Synthase (EC 4.2.1.52) (DHDPS). - <i>Bacillus Subtilis</i> .	1	-CAT	TTA~		179		457	Reverse
379.	Unknown	2	-CAT	TCA~		104		322	Reverse
380.	Unknown	2	-CAT	TCA~		248		649	Reverse
381.	Unknown	1	-CAT	TTA~		56		394	Reverse
382.	Unknown	2	-CAT	TTA~		254		409	Reverse
383.	Unknown	1	ATG	TAG		138		617	Forward
384.	Unknown	2	-CAT	TTA~		225		479	Reverse
385.	Unknown	2	ATG	TAA		747		857	Forward
386.	Unknown	1	ATG	TAG		294		443	Forward
387.	Unknown	2	ATG	TGA		356		544	Forward
388.	Unknown	1	-CAT	CTA~		4		141	Reverse
389.	Unknown	1	CTG	TAG		1		579	Forward
390.	Unknown	2	-CAT	TTA~		309		452	Reverse
391.	Phosphopentomutase (EC 5.4.2.7). - <i>Escherichia Coli</i> .	1	ATG	TAA		3		233	Forward
392.	D-Alanyl-D-Alanine Carboxypeptidase Precursor (EC 3.4.16.4) (DD-Peptidase)(DD - Carboxypeptidase)(Cpase)(PBP5). - <i>Bacillus Subtilis</i> .	1	-CAT	TTA~		52		537	Reverse
393.	Na+ and Cl-dependent gamma-aminobutyric acid transporter homolog- <i>Haemophilus</i>	1	TTG	TGA		2		268	Forward

	influenzae (strain Rd KW20)						
394.	Unknown	2	ATG	TGA	319	546	Forward
395.	dihydrolipoamide dehydrogenase (EC 1.8.1.4) - Pelobacter carbinolicus	1	ATG	TGA	3	284	Forward
396.	Unknown	2	ATG	TGA	241	450	Forward
397.	Beta-Glucosidase A (EC 3.2.1.21)(Gentiobiase)(Cellobiase)(Beta-D-Glucoside Glucohydrolase). - Clostridium Thermocellum.	1	ATG	TAA	184	453	Forward
398.	Uracil Permease. - Bacillus Caldolyticus.	1	ATG	TAA	93	353	Forward
399.	Unknown	2	ATG	TAG	127	516	Forward
400.	ligoendopeptidase F- Lactococcus lactis	1	ATG	TGA	134	310	Forward
401.	Stratpasea NCBI gi: 153565NCBI gi: 4- Streptococcus Faecalis DNA.	2	ATG	TAA	392	568	Forward
402.	Unknown	2	ATG	TAA	376	507	Forward
403.	Exodeoxyribonuclease Small Subunit (EC 3.1.11.6) (Exonuclease VII Small Subunit). - Escherichia Coli.	2	-CAT	TCA~	470	682	Reverse
404.	ATP-Depeent DNA Helicase RECG (EC 3.6.1.-). - Escherichia Coli.	1	ATG	TGA	3	455	Forward

SEQ ID NO:	Identity	ORF #	Codon		Position		Direction
			Start	Stop	Start	Stop	
405.	Possible thiamin biosynthetic enzyme	1	-CAT	TTA-	15	347	Reverse
406.	SPOU Protein. - Escherichia Coli.	2	ATG	TAA	322	618	Forward
407.	Malonyl Coa-Acyl Carrier Protein Transacylase (EC 2.3.1.39). - Escherichia Coli.	1	ATG	TAG	85	498	Forward
408.	Unknown	1	-CAT	CTA-	17	118	Reverse
409.	nucleoside diphosphate kinase (ndk) homolog- Haemophilus influenzae (strain Rd KW20)	1	CTG	TGA	1	159	Forward
410.	Nucleoside Diphosphate Kinase (EC 2.7.4.6)(NDK) (NDP Kinase). - Escherichia Co LI.	2	ATG	TAG	215	481	Forward
411.	Unknown	1	-CAT	TTA-	21	368	Reverse
412.	Unknown	2	-CAT	TCA-	162	314	Reverse
413.	Unknown	1	ATG	TAA	187	417	Forward
414.	Unknown	2	ATG	TGA	316	417	Forward
415.	Unknown	1	ATG	TGA	316	453	Forward
416.	Enolase (EC 4.2.1.11)(2-Phosphoglycerate Dehydratase)(2-Phospho-D0Glycerate Hydro-Lvase). - Bacillus Subtilis.	1	-CAT	TTA-	4	435	Reverse
417.	Unknown	1	CTG	TGA	1	363	Forward
418.	Unknown	1	ATG	TGA	39	383	Forward
419.	PILB Protein. - Neisseria Gonorrhoeae.	1	-CAT	TTA-	145	327	Reverse
420.	Unknown	2	ATG	TGA	285	533	Forward
421.	Unknown	1	CTG	TAG	2	379	Forward
422.	integrase/recombinase (xprB) homolog - Haemophilus influenzae (strain Rd KW20)	1	ATG	TAA	305	421	Forward
423.	Unknown	1	-CAT	CTA-	173	436	Reverse
424.	Unknown	1	-CAT	CTA-	182	427	Reverse
425.	Unknown	1	ATG	TAA	49	372	Forward
426.	"Mutator Mutt Protein (7	1	-CAT	CTA-	21	446	Reverse
427.	Unknown	1	ATG	TGA	177	380	Forward
428.	Possible phosphatase	1	ATG	TAG	112	402	Forward
429.	Unknown	1	ATG	TGA	110	271	Forward
430.	Phosphoenolpyruvate Carboxylase (EC 4.1.1.31). - Corynebacterium Glutamicum.	2	ATG	TGA	337	561	Forward
431.	Unknown	1	ATG	TGA	214	324	Forward
432.	50S Ribosomal Protein L31. - Bacillus	1	ATG	TAA	142	426	Forward

	Subtilis.						
433.	glycosyl transferase (IgtD) homolog - Haemophilus influenzae (strain Rd KW20)	1	ATG	TGA	127	399	Forward
434.	Unknown	2	-CAT	CTA~	244	435	Reverse
435.	Unknown	2	ATG	TGA	118	309	Forward
436.	Factor essential for Expression of Methicillin Resistance. - Staphylococcus Aur Eus.	2	-CAT	TTA~	168	434	Reverse
437.	Unknown	1	-CAT	TCA~	2	214	Reverse
438.	Unknown	1	TTG	TAA	2	142	Forward
439.	Unknown	1	ATG	TAA	30	191	Forward

SEQ ID NO:	Identity	ORF #	Codon		Position		Direction
			Start	Stop	Start	Stop	
440.	Aspartate Aminotransferase (EC 2.6.1.1) (Transaminase A)(ASPAT). - Bacillus SP. (STRAIN YM-2).	1	-CAT	TCA-	63	416	Reverse
441.	Unknown	1	ATG	TAA	52	342	Forward
442.	Unknown	2	-CAT	TCA-	210	455	Reverse
443.	Unknown	1	TTG	TGA	2	517	Forward
444.	ATP-Dependent DNA Helicase RECG (EC 3.6.1.-) - Escherichia Coli.	1	ATG	TGA	83	376	Forward
445.	Unknown	1	ATG	TAA	70	384	Forward
446.	Cell Division Protein FTSA. - Bacillus Subtilis.	1	TTG	TAA	3	371	Forward
447.	Unknown	1	ATG	TAG	70	441	Forward
448.	Unknown	1	ATG	TAG	104	454	Forward
449.	Unknown	1	CTG	TAA	1	159	Forward
450.	Unknown	1	ATG	TAA	120	347	Forward
451.	Unknown	1	ATG	TGA	31	423	Forward
452.	Unknown	2	ATG	TGA	225	416	Forward
453.	Unknown	1	ATG	TGA	290	418	Forward
454.	Unknown	1	ATG	TGA	3	269	Forward
455.	JAG Protein (SPOIJJ Associated Protein). - Bacillus Subtilis.	1	ATG	TGA	93	365	Forward
456.	"DNA -3-Methyladenine Glycosidase I (EC 3.2.2.20)(3-Methyladenine-DNA Glycosylase I	1	ATG	TAG	91	282	Forward
457.	"Glucan I	1	-CAT	TTA-	4	150	Reverse
458.	Unknown	1	-CAT	CTA-	245	400	Reverse
459.	Glutamate/Aspartate Transport ATP-Binding Protein GLTL. - Escherichia Coli.	1	-CAT	TCA-	81	218	Reverse
460.	Unknown	1	-CAT	TTA-	103	492	Reverse
461.	Unknown	1	ATG	TGA	305	484	Forward
462.	Unknown	1	-CAT	TCA-	29	355	Reverse
463.	Unknown	2	-CAT	TTA-	572	838	Reverse
464.	Unknown	2	-CAT	TCA-	652	1026	Reverse
465.	Unknown	2	-CAT	TTA-	318	764	Reverse
466.	Unknown	2	ATG	TGA	719	805	Forward
467.	Llcpyrda NCBI gi: 511014 - Lactococcus lactis.	1	ATG	TGA	134	472	Forward

468.	Unknown	1	ATG	TGA	385	492	Forward
469.	Unknown	2	ATG	TAA	587	721	Forward
470.	galE protein - Neisseria meningitidis	1	-CAT	TCA-	23	460	Reverse
471.	Unknown	2	-CAG	TTA-	717	1319	Reverse
472.	Naphthoate Synthase (EC 4.1.3.36) (Dihydroxynaphthoic Acid Synthetase)(Dhna Sy Nthetase). - Escherichia Coli.	1	ATG	TGA	97	414	Forward

SEQ ID NO:	Identity	ORF #	Codon		Position		Direction
			Start	Stop	Start	Stop	
473.	Unknown	1	CTG	TGA	1	246	Forward
474.	Unknown	1	-CAT	TCA-	341	748	Reverse
475.	Unknown	1	-CAT	TTA-	217	858	Reverse
476.	Unknown	1	-CAT	TTA-	499	729	Reverse
477.	Multiple Sugar-Binding Transport ATP-Binding Protein MSMK. - Streptococcus MUTA NS.	2	ATG	TAA	407	571	Forward

Table 2 shows the correlation between the SEQ ID NO of each DNA sequence of the invention with the SEQ ID NO(S) of polypeptide or polypeptides that its open reading frame(s) encodes. For example, the DNA of SEQ ID NO:1 encodes one polypeptide, that of SEQ ID NO:224. Whereas, the DNA of SEQ ID NO:2 encodes two polypeptides, the polypeptides of SEQ ID NO:225 and SEQ ID NO:226.

TABLE 2

DNA	Protein (open reading frame)
===	=====
1	224
2	225,226
3	227
4	228,229,230
5	231
6	232
7	233
8	234
9	235
10	236
11	237
12	238
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16	242
17	243,244
18	245
19	246
20	247,248
21	249,250
22	251
23	252
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25	255,256
26	257
27	258
28	259
29	260,261
30	262

31	263
32	264
33	265
34	266
35	267
36	268,269
37	270
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42	275
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54	288,289
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63	301
64	302,303
65	304,305
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71	311
72	312,313

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79	324,325,326,327
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83	331
84	332
85	333,334
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88	337
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91	340
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93	342
94	343
95	344,345
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211	462,463
212	464
213	465
214	466
215	467
216	468,469
217	470,471
218	472
219	473
220	474
221	475
222	476
223	477

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Black, Michael

Hodgson, John

Knowles, David

Nicholas, Richard

Stodola, Robert

(ii) TITLE OF THE INVENTION: Novel Compounds

(iii) NUMBER OF SEQUENCES: 477

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SmithKline Beecham Corporation

(B) STREET: 709 Swedeland Road

(C) CITY: King of Prussia

(D) STATE: PA

(E) COUNTRY: USA

(F) ZIP: 19406-0939

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette

(B) COMPUTER: IBM Compatible

(C) OPERATING SYSTEM: DOS

(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: 01-APR-1997

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/014690

(B) FILING DATE: 02-APR-1996

PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/025788

(B) FILING DATE: 22-AUG-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Gimmi, Edward R

(B) REGISTRATION NUMBER: 38,891

(C) REFERENCE/DOCKET NUMBER: P50466

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 610-270-4478

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(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 683 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCAAACATG GTCTCTTCTA GTTGCATGGT CGCAATCGGA TCCAAGGCTG AGGCTGGGCT	60
CATCCATTAA GAGGATATCT GGCTTAACAG AGATGGCAGC AGCGATACAG AGACGTTGTT	120
GCTGACCACC TGATAAGGTC AAGGCTGACT TGTGGAGATC GTCTTTAACC TGATCCCAAA	180
GGGCAGCCTG ACTAAGGGAG GTTTCTACGA TTTCATCTAG GACTTGCTTA TCCTTAACTC	240
CAGCACGTTC ATGCGCAAAG GTAATATTAC GGTAAATTGA CTTAGCAAAT GGATTGGGGC	300
GTTGAAAAAC CATTCCAATG TGTTTACGCA TTTCATAAAC GTTGATTTCT GGACGGTTGA	360
CATCAATTCC ACGATAGAGA ATCTGCCCCG TTAAGTTAGC AATATCAATG GTATCATTCA	420
TGCGATTGAG ACTGCGTAAG TAGGTAGATT TCCCCGATCC CGACGGACCA ATCAAAGCTG	480
TAATTTTATT TCCTTTCAAA TTGCATATCA ATCCCCCTAA TGGATTTCATT TTTACCATAG	540
TAAACATGGA CATCCTTAGT AGAAAGGGCT ACTTTTCTT CAGGAAAGGT AAGGATATGC	600
TTCTCATCCC AGTTATATGT TGACATGGCT TCTCCTTTAG GCACGGTTA ATTTCTTGTC	660
TAGATAGCTT CCGAACTTAC GAG	683

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1512 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTAGTCCAAC	TAAGTGAGTT	TTCCTTTATC	TATTATATCA	AATATAAGTC	CGTTTGTAAC	60
TAGTGAAGAA	TTCTTTTGTC	CGCTCTTCTT	TAGGGGTGTG	GATAATCTCA	TCCGGAGTTC	120
CAGACTCGAT	GATTTTCCCC	TTATCTAAGA	AGAGAAATTT	ATCCGCAACT	TGGGCTACAA	180
AGGGCATGTC	ATGACTGACC	AAAATCATGG	TCTGACCTGA	CTTAGCAGCA	TCTGCAATAG	240
ACTTTTCTAC	TTCAACGACC	AATTCTGGGT	CAAGGGCTGA	AGTTGGTTCG	TCTAAGAGCA	300
AAACATCTGG	TTTCATAGCA	AGCGCACGCG	CTAGGGCAAC	CCGTTGCTTC	TGTCCACCTG	360
ATAAATGGCG	AGGATAATGG	TTTTACGGT	CCGAAAGCCC	AACCTTAGCC	AACCTTTCCT	420
TGGCAATCTT	AGTCGCTTCT	TGGTCAGATA	ATTTCTTGAC	AACAACCAAG	CCTTCTTTCA	480
CATTATCAAG	TGCTGTTTCG	CGTTCAAATA	AATTAACTG	TTGGAAAACC	ATAGACAAC	540
TACGGCGTAG	GGCAAGGATT	TCTTCTTGAG	TGATTTTGA	AAAATCAACT	GAAAAACCAT	600
CAATCTGAAT	AGAGCCACTG	TCAGGTGTTT	CAAGATAATT	GAGACTGCGA	AGAAAGGTTG	660
ATTTTCCAGC	TCCTGAAGAA	CCAATCAAGG	CTACAACCTC	CCCTTTTGA	ATATCCAAGT	720
TCAGATGATC	CAAGACAGTC	TGTCCTGAAA	AGGATTGCT	TAAATTCGAA	ATCTTAATCA	780
TTAACGAAGG	TCTCCTTTCA	CATCTGTTTG	CACTGTATCA	GGTGCAGAAA	TAGCCATTTT	840
TCTCTCGATG	AAACGACCGA	GGCTTTCAAT	TCCGATATTG	ACTACCCAAT	AAACAAGGGC	900
AACAGAGATG	AAGCGTTCAA	AATAGCGATA	ATCAGCTCCA	CCTAGAATCT	GAGCTTGGGC	960
AAAGACTTCC	ACAACACCCG	CACTAAAAGC	TAGAGATGTT	CCCTTGGTCA	AACCGATGAG	1020
GGAATTAATC	AAGGTTGGAG	TAGCTACCAC	CGCTGCATTA	GGAATAATCA	CTCGTCGATA	1080
AACTTGCGCT	CGGGTCATAC	CCAGACTGCG	CGCCGCCTCA	ATCTCACCAG	GATTAATCTGA	1140
GAGAATGGCT	GCACGAATGG	TTTCACTAGC	ATAAGCTGCC	TCATTAAAGG	CAAAAGCGAC	1200
AATCGCAAAA	GCTGCAGCTG	GAATCGCATT	GATATTGAGA	CCAGTTCCCC	ATTGCTGATT	1260
GAGGGCTTTC	AAAGCCAAAG	GGATTCCGTA	GTAGGTCAAC	ATGAGTTGCA	CCAAAATCGG	1320
TGTCCCTTTT	AAGAACTAA	CAAAGAAGGC	CTGCAAGGGA	TATAAAATCT	TGACACGATT	1380
GATCTTCACA	ATGGCAAAAA	GAAGCGCCAA	AACCAAGCCA	AAAAGGGCAC	CGCCAATTGT	1440
CAACATAATT	GTTGTTGGAA	GTTGTTGGAC	AATTCTAGGG	ATTCCATCAA	AGACCGAACG	1500
TAGGCTAAAC	AG					1512

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGGAGATTA	TTGAGATTGC	CCGTCAAAAC	GATTTGATTA	TNTTTGCGGA	TGAAATCTAT	60
GACCGCATGG	TAAATGGACG	GACATGTGCA	TAACGCCTGT	GGCGAGCTTG	GCACCAGATG	120
TCTTCTGTGT	CAGCATGAAT	GGTCTGTCAA	AATCCCACCG	CATAGCAGGT	TTCCCGTGTG	180
GGATGGATGG	TCTTGTCTGG	CCCTAAGACT	CATGTTAAGG	GCTATATCGA	AGGGCTCAAT	240

ATGCTGTCCA	ATATGCGCCT	TTGCTCTAAC	GTTTTGGCTA	CCAACGCTGC	ATTAGGAATA	300
ATCACTGTCTG	TACAAACTTG	CGCTTGGGGG	GTCACCAATC	AGTCGATGAA	TTGCTTCTTC	360
CTGGTGGACG	AATCTACGAG	CAAAGAAATT	TCATCTATAA	TGCCATTCAA	GATATTCCAG	420
GTTTGTCTGC	CGTTAAACCC	AAGGCGGGGC	TCTATATCTT	CCCAAAAATC	GACCGCAATA	480
TGTACCGTAT	CGATGATGAT	GAGCAGTTTG	TCCTTGATTT	CTTGAAGCAG	GAAAAGGTTT	540
TCTTGGTTCA	TGGTCGAGGC	TTTAAC TG GC	AGGAACCAGA	CCACTTCCGT	ATCGTTTACC	600
TTCTCGTGT	TGATGAGTTA	GCCCAAATCC	AAGAAAAGAT	GACTCGTTTC	TTGAAACAGT	660
ATCGTAGATA	GGGCTTGCAT	TCGAAAAAGC	TGGAAACATT	TGCCTAGAG		709

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTGCTTCAGA	ACCTGCCAAA	CCAGCACCGA	TAACATTGAT	ATAAGATTGA	GACACGACAC	60
TAATACCTCT	TTGGGAGTGT	GAAGTTAAGA	TTACATTGTA	AAAAGCCAAT	CAGACTTACA	120
AGCTTTTCGAG	TTTCTTGGCT	CAGGCTGAAA	AAGTCCACAG	GGCTTTTNCA	CTCCCACAAA	180
TCTTTCTATT	TTTTCTNCTA	CTAGTATAAC	AAAAAAAGGG	AAGAAGGNAA	ACTTCCCTGT	240
TTAGTCATTT	TCTTGATGTA	AAGAGATAGT	GAGTATTCCA	GTTAAGAATC	AATTATATGC	300
TACTCTATAA	AATCTTTTCC	ACATAACGGA	TCGATAGGGA	CTGTTATTCT	ATCTCTTGCT	360
ATAACCGTAT	TATCTAAAC	AGCATAACAT	TCAACATAGT	GATCTCCTTT	AAACTGTGAA	420
TCTTCCGTGA	TATTTTATTT	TACCTGAAAA	AATAGCACAC	GCTCACAATT	CTTCCTAATA	480
GCCTCAGCTT	CAATATTTCT	TACTTTCCAA	TAGACTCCCT	GCGAAACAAA	ATATGGTATA	540
GTAGTTCTAT	GAATGATGAA	GCAAGTAAAC	AACTAACTGA	TGCACGATTT	AAGCGTCTTG	600
TTGGTGTTC	GCGCACGACT	TTTGAAGAGA	TATTAGCTGT	ATTAAAAACA	GCTTATCAAC	660
TTAAACACGC	AAAAGGTGGA	CGAAAACCTA	AATTAAGCCT	AGAAGACCTT	CTTATGGCCA	720
CTCTTCAATA	TGTGCGAGAA	TATCGAACTT	ATGAACAAAT	TGCGGCTGAT	TTTGGTATCC	780
ACGAAAGCAA	CTTAATCCGT	CGGAGCCAAT	GGGTGGAAGT	AACTCTTGTT	CAAAGTGGTG	840
TTACGATTTT	AAGAACTCCT	CTCAGTTC TG	AGGACACGGT	AATGATTGAT	GCGACGGAAG	900
TACAAATCAA	TCGCCCTAAA	AAAAGAATTA	GCGAATCATT	CTGGTAAAAA	GAAATTTTAC	960
GCTATGAAGG	CTCAAGCGAT	TGTCACAAGT	CAAGGGAGAA	TTGTTTCTTT	GGATATCGCT	1020
GTGAACTATA	GTCATGATAT	GAAGTTGTTC	AAAATGAGTT	GCAGAAATAT	CGGACAAGCT	1080
GGAAAAATCT	TGGCTGATAG	TGGTTATCAA	GGGCCCATGA	AGATATATCC	TCAAGCACAA	1140
ACTCCACGTA	AATCCAGCAA	ACTCAAGCCG	CTAATAGCTG	AAGATAAAGC	TTATAACCAT	1200
GCGCTATCCA	AGGAGAGAAG	CAAGGTTGAG	AACATCTTTG	CCAAAGTAAA	AACGTTTAAA	1260
ATGTTTTTCAA	CAACCTATCG	AAATCATCGT	AAACGCTTCG	GATTACGAAT	GAATTTGATT	1320
GCTGGCATT	TCAATTATGA	ACTAGGATTC	TAGTTTTGCA	GGAAGTCTAT	TATTTTCCTT	1380

ATTGTCCTGTA AGTCTACTGA CCTTGTTGTT TATCCCAGTC ATGGTTTCTA GTTCGGGCTC	1440
AGAGTTTCAA AGTGGATGGC AAGAGCATCA ATTGATTGCT GAGAAGGTTA GTAAAACACT	1500
TGACAAGACA TTTGATAAGG ATGTCAGAAA AATTCCGACC AGTCCAGTTT TATCAAAAAT	1560
TTGTAGATGA GATGGGAAGG ATTTACTC	1588

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTGTTTTTAA TACAGCTAAC ATCTCTTCAA AAGTGGTACG CTGAACACCA ACAAGACGCT	60
TAAATCGTGC ATCAGTTAGT TGTTTACTTG CTTTCATCATT CATAGAACTA CTATACCATA	120
TTTTGTTTCG CAGGGAGTCT AATATTGTCA AATACTGGAG CGCTCATTGC TGGTATACGG	180
AATAAGATTG GCCCAGCTTC GATAACTGGG ATACCTGGTT CAAAACCAAG ATCTGTTGCA	240
GCGATTGGTG TAAAGATATC GTAACCTTTC ATAAGGTCTT CGTTTACATC TTTCACCATG	300
ACTGCATCAC AGTGAACATC ATAACCACGG TTTGAAAGTT CTTCTTCTAG AGCACTTTTA	360
ATTTGGTGAC TTGAGTTAAC ACCTGCACCG CAGGCAGCAA GAATTTTAAT CATTTAGATT	420
TCCTCCGATT TTATTTTTTA ATAGACAAGA TTAAGCGGTT GCTTCAGCAA TGTAAGCATA	480
AAGTTTTTCT GGTTCGAAA TTTTGTAGTAG GTCTTCAAGA TGTCATTTC CTGTGAAAAA	540
GTCCATCAAC TGAGCCAGAA TATTTGTTT ACTTGAAGTT GAGTTATTGA TGATAAAGAA	600
GAGCAAGGAT ACTTCTACTT CTTATCAGG AGCTATCATA TTGTGAAAAG TTAGTGATTT	660
TTCTAATCGA ACAACCACCA CTTTTCTCAG	690

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ACTGCTACCT TTAAGAAGAT AGTAGACGTA TATACTTTTT TAAGAAAATC AAAAAGATAC	60
TATAAAAAAT CTATTGTTT ATTGAATTTA AGACTTTGGT AACAAATTGA AAATAAAAAG	120

GAGGTATTCA TCATGAATAC AAAAATGATG TCACAATTTT CTGTTATGGA TAATGAAATG	180
CTTGCTTGCG TTGAAGGTGG AGATATTGAT TGGGGAAGAG AAATTAGTTG TGCAGCAGGG	240
GTTGCATATG GCGCAATTGA TGGGTGTGCA ACAACGGTTT GATATTTCTA TTGGGACCAT	300
TTGCTATAGG AATAGGTGTA ACTGGTGCTG CAGGTGGAG	339

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTGAAGACCT CGTGCTACTC CTCCTCCAAC ACCTGCTTTG GCAAAATCTC CCCAATTGCA	60
TCCGCCACCT TCAACTCAAG CAAGCATCTC AGTATCCATA ATTTCAAATT GTGACATCTT	120
TTTTGTATTC ATAACGAATA CCTCTTTTTT ATTTTAAATA TTTGTCTTGT TACAAACTTG	180
ACAAGTTTAG TATAACAGTA TCTATTAATT TTTTTCATCC AAATCTTGAA TTGGCATCGA	240
AACGTCTTGA ATTAGCTTTT TTGTTTCAAA ATCATCTCTA TTTTAAAAA AGATGTTTTTC	300
TAATCACTTT TTTACTATTT AGACTTCCTG CAAAAC TAGA ATCCTAGTTC ATGATTGATA	360
ATACCAGCAA TCAAATTCAT TCGTAATCCG AAGCGTTTAC GATGATTTTCG ATAGGTTGTT	420
GAAAACATTT TAAACGTTTT TACTTTGGCA AAGATATTCT CAACCTTGCT TCTCTCCTTA	480
GATAGCGCAT GATTACAGGC TTTATCTTCA ACTGTTAGCG GCTTGAGTTT GCTGGATTTA	540
CGTGGAAGTT TGTGCTTGAG GATATATCTT CATGAGCCCT TGATAACCAC TGTCAGCCAA	600
GATTTTACCA GCTTGTCGGA TATTTCTCAT TTCTAAAAAC CATCTACTTC CGTTGACTTG	660
GAAGTCCGAT TGCTATTTTC CTTGAATGAT TTAAACCACA TCTCCTACAC TTTGGAGTTG	720
GTCAATTTCC TCATCGCTGA TTTCGATACT AAATTCATCC TCCAGCGTCA AGATAAACTC	780
CATCAAATCA ACTGAGTCAG CATCCAAGTC GTCTTTCAGA CTCAAGGATT CTGTCACGAC	840
AAAGTCCTCT CCCTGTCGCT CTTGGATAAT GGTCAACAATA CTGTCAAAAA TTTCTTTTTC	900
TCTCATCTCT TTTATTCTCC TGAAAATTCA CGCGCAGTCT GGGCAACTAC TTCTGTTTCT	960
AGCATGGTAC GAATCTGGCG AATCGTACTA TAAACAGCCT TGGCATCGCT TGAGCCATGA	1020
GTCTTGACAA CAGGTGCCTT GACACCAAAC AAGACCGCTC CACCAACATC TGAATAATTG	1080
AGCTGTTTTT TCAAACCTCT GAGGCTGTCC TTGAGAAGGA GGGCACCTAG TTTGCTCGA	1140
AGACCACCAC CTGTAATAGC TGTCTTGAGC AAGCCCATGA TTCCCATAGC TGTCCCTTCG	1200
ATGGATTGGA GCACAGCGTT TCCCGTGAAG CCATCTGCCA CAACAACATC TGCAACGCCA	1260
TTTCATCAAAT CACGCGCTTC CACGTTTCCG ATAAAGTTCA AACTTTCATC AGCCGCCAGT	1320
AATTCATAAG TTTCTTTACG AAGCGGGTCG CCCTTGCTAC TCTCTGTTCC GTTGTGAGC	1380
AAACCAACAC GTGGTTGCGC AATGCCACGA ACATTCTTGG CATAGAAAGA ACCTAGGACA	1440
GCGTATTGAT GGAGGTGCTG GGCTGTATTT TCTGCATTAG CACCGAGGTC AAGCATGTCA	1500
AAACCTTTCC CATCTACAGT CGGCAATGTT GACATAAGTC CAGGACGGTC GATATTCTTG	1560
ATACGACCCA CGATGAAGAA TCCAGCAGCC AACAAAGCAC CTGTATTCCC AGCCGAAAGG	1620

ACAGCGTCTG CTTACCATC TTTGACAGCC TTGGCTGCCA ATACCATACT GGCATTTTTC 1680
 TTATTCCGAA TAG 1693

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTAAATCTGC TTGCTTAGTC CACTTGCTTG AGCCAAGGAG TCACATACTC AAAATTTTCA 60
 TGAAAGTCAT AGGTACCGTC TTCTTTTFTA GCTGAAAAGA AAAGTCCATC GTGGTAGAGC 120
 AAATCCCCGT GGGCCATAAT TCTGGCAGTT TTTTCCTCTT CCTACTCCTG AGACTTTTGC 180
 TTAGTCCCCT CTTGAGAAAT AGTATCTCGT TTTTGACTAG TCAAGGGATT CCTTGGAAGC 240
 TTTCAAACAA CAAGACCAAG CCCATTGATA AACCAACTGC TAGCAAGAGT ATCGCCACAA 300
 ATCCCTTATT GCTCCACTTG CGATAACTCC TAAAAAGTTT ACCAAGCCCT TCATAAAACG 360
 AAAAGCTAAA CCACCCTGAT TTCGATTTTG TCTTCTTTGT ATCTTCGTTT TCCCTACTTT 420
 CTTATGCAAG CCTTTTCTTT TTATTATATC ACAGATAAGT ATTTCTTTCA CAATTGAATT 480
 GAACTTCCCA TCTATTTTCT ATAAATCCTA AATGCCATAA TGCTTTCAAT TCCTGTCATT 540
 TTGTGATATC ATGTAGAAGA AATGAATAA TCCACAGTGG CTTATTCCAA GTATACCACT 600
 TGGGCTTTGG CAGTAG 616

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1973 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTAATATAGA ATAATCACCG CCGTTGTGAA AGAACGATTG GATGATAATC CAATCGTTCA 60
 GGGAAATTGG AAGACCTTGG GTTTCCAATT TAGGCATGAG ACACCTTTGG TGGCTGCTGC 120
 CGTCCCTCAC AAGCTAAGGT GATTGTTGAA AAAGAGGAAA AAGGAGAAGA AATGAAACCA 180
 GTAATTTCCA TCATCATGGG CTCAAAATCC GACTGGGCAA CCATGCAAAA AACAGCAGAA 240
 GTCCTAGACC GCTTCGGTGT AGCCTACGAA AAGAAAGTTG TTTCCGCACA CCGTACACCA 300

GACCTCATGT	TCAAACATGC	AGAAGAAGCC	CGTAGTCGTG	GCATCAAGAT	CATCATCGCA	360
GGTGCTGGTG	GCGCAGCGCA	TTTGCCAGGC	ATGGTAGCTG	CCAAAACAAC	CCTTCCAGTC	420
ATTGGTGTGC	CAGTCAAGTC	TCGTGCTCTT	AGTGGAGTGG	ATTCACTCTA	TTCTATCGTT	480
CAGATGCCGG	GTGGGGTGCC	TGTTGCGACC	ATGGCTATCG	GTGAACTCTT	TTTTAGGATA	540
TAAAACAGGG	TTCGGATAAG	TTTTTTTGCA	AGGTGGATGA	TGGCTACATT	GTAATGTTTT	600
CCTTATTCTA	ACTTAGTCTT	AAGATAGGTC	TTAAAACCAG	GTGAAAAGCG	AAGGCATGCT	660
TTGGCAGCTT	GTATGAGTAC	CTACCGCAGA	TGAAGGGAAC	CCCGTTTGAC	CATCCTTCCA	720
ACTAAATCAA	TCTGACCTGA	CTGATAAATA	GAAGAATCCA	GTCCAGCGAA	AGCTTGTAAT	780
TGAGCAGGAT	TATCAAAGGC	ATGAATATTT	CGAATCTCGG	CTAAAATGAC	CGCCCCATAA	840
CGATTCTCAA	TCCCAGTAAC	CGTCGTGATG	ACCGAGTTTA	ACTCAGCCAT	CAAGTCATTG	900
ACACATTTTT	CCGCCTTGTC	AATGAGCCTC	TTGTAATGTT	TGATGTTTTT	ATTACACGAG	960
ATAAACGTC	TATGCGTTAT	CAAACCTCATT	ACCAATTAAA	ACAAATGTGG	TTAGATCCTT	1020
TCGGAAATTG	TCAAGCGATT	GGAGGAAATG	AACTAATCCA	CAGCGGCTTA	TTCCAAGTAT	1080
ACCACTTGGG	CTTTGGCAGT	AGCTAACTGC	GCTAAATATA	ATATAAGGAG	GAGTAAAATG	1140
AAGACAGTTC	AATTTTTTTG	GCATTATTTT	AAGGTCTACA	AGTTCTCATT	TGTAGTTGTC	1200
ATCCTGATGA	TTGTTCTGGC	GACTTTTGCC	CAAGCCCTCT	TTCCAGTCTA	TTCTGGACAA	1260
GCGGTGACGC	AGCTAGCCAA	TTTAGTTCAA	GCTTATCAAA	ATGGGCAATC	CAGAACTTGT	1320
ATGGCAAAGC	CTATCAGGAA	TTCATGGTCA	ATCTTGGCCT	GCTGGTTTTG	GGTCTATTTT	1380
ATCTCTAGGT	GTAATATAAA	CATGTGTCTC	ATGACGCGCG	TGATTGCAGA	ATCGACCAAC	1440
GAGATGCGCA	AAGGTCTCTT	TGGTAAGCTT	GCTCAGTTGA	CGGTTTCTTT	CTTTGACCGT	1500
CGACAAGATG	GCGATATCCT	GTCTCATTTT	ACCAGTGATT	TGGATAATAT	CCTCCAAGCC	1560
TTTAACGAAA	GCTTGATTCA	GGTCATGAGC	AATATTGTTT	TATACATTGG	TCTGATTCTT	1620
GTCATGTTTT	CGAGAAATGT	GACGCTGGCT	CTCATCACCA	TTGCCAGCAC	CCCATTGGCT	1680
TTCTTATATG	TGATTTTTCAT	CGTGAAAATG	GCACGTAAAT	ACACCAACCT	CCAGCAGAAA	1740
GAGGTAGGGA	AGCTCAACGC	CTATATGGAT	GAGAGCATCT	CAGGCCAAAA	AGCCGTGATT	1800
GTGCTAGGAA	TTCAAGAGGA	TATGATGGCA	GGATTTCTTG	AACAAAATGA	GCGCGTGCGC	1860
AAGGCAACCT	TTAAAGGAAG	AATGTTCTCA	GGAATTCTTT	TCCCTGTCAT	GAATGGGATG	1920
AGCCTGATTA	ATACAGCCAT	CGTCATCTTT	GCTGGTTCGG	CTGTACTTTT	GAA	1973

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTAAACCAAT	AGTTGCTGAA	GACCATAATC	CAGCTGCTGT	TGTTAAACCT	TTAACTTTTT	60
GATTAGTTAC	CATGATTGTT	CCTGCCCTTA	GGAAACCCAA	GCCACTAATT	ACTTGGGCTC	120
CCATTGCACT	AGGATCACCG	CTACCATAAC	GACTAGTGAT	GAAGTGATTT	GTCATCATTA	180

CAACACAAGT TCCCAAACAA ACTAGTAAGT AGGTTCTAAT CCCTGCTGCT TGGTTTTTTGA	240
CTCCTCGCTC ATAGCCAACA ATGCCACCGA AAAGAATCGC TAAAAAGCAC CTAAGAAGTA	300
TTTCCCAAAT ACTCAGTTCG TATGAAAGAT TCATATTATC TCTTACCTCG TTTACCTTGG	360
AATAGGCTTG ATAAATAAAG AGCTGCACTA GACATAATCA TTAAAATTAC AGAATAAACA	420
AACATCATTG CCTGTGCATT TAAAGTTGCT GTTTCATCAG TAGACTGTTT AATAACGATT	480
CCCAATGGTT GGAAAAGTGG ATGGTACAAG AATACAGATA AGTCATAGTC AGATAATAAA	540
GAATTAAAGT TTAACACAAC TACTGATAAT ACGACTGGTA AAATATACGG TATAATAACT	600
CGCACCATAG TGTAGAACT AGATGCACCC ATACTACGTG CAGCTTCTTC CATATCATTA	660
TCTATACTGA AAAATACAGC CCGAATCATT CTATAAGAAA ATGGTAATTT TTGAATAGTA	720
TATGCAATAA GTAAAATAAT TACTGTTCCT ACTAAACTA AATTAAATAG TATTAAATGA	780
GGTATATTAT AAGTGAACAT TAATCCTAGT GCAATCAATG TACCTGGCAA TATCCATGGT	840
ATCAGTGCAC CATACTCAA GAATTTATCG AACTTACTCT TGTTTTTATG TACAATACGT	900
GAAATTACTA TTGCTATAAT TGTAGCAATT ACCGCAGCTA AAATTGCATA AACAACGCTG	960
ACTAGGTAAG GACGAAATGA TTGAGCATCT GTAAATAAAT TAGCATAGTT CGCTAACGTA	1020
AATTTAGATA GATCTAAAGT TCCCGTCTTG ATCGTCAACG AGTCTGTAAA CGAGTATAGA	1080
ATTATCAAAA CTATTGGTAA CATATAGATT GCAAACAATA CATACGCAGC AATGTGAGCA	1140
AGAATTATTC CATAATGGAG AAGAAAATTA TCTGCTTCCT TAATACTAGC CTGGTTTTCG	1200
AAACAGAAT	1209

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTAAGTCCTT TTAGTTTTAT CTTAATTCTC TTATTGTTGT AATAATCAAT ATAGTCTATA	60
ATGGCTTGTT CCAATTGCTT AAGCGACTGA AACGACTTCT CATAACCGTA AAACATTTCC	120
GATTCAGAA TCCCAAAGAA AGATTCCATC ATACCGTTGT CTTGGCTGTT TCCCTTGCGT	180
GACATAGATG CTGAATTCC CTTACTCTTA GGAACCGATG ATAAGAATCG TGTTGGTATT	240
GCCAGCCTTG GTCACATATGG AGAATCGTAT TCTCGTAGTG CTTCTCTGTG AATGCCTGTT	300
CCAACATTGT TTGTACTTGT TCTAAGTTGG GTGAAGTTGA AAGATTATAG GCGATAATTT	360
CGCTATTAAA GCCATCTAAA ACTGGTGATA AGTAAAGCTT TTGAGTACTT GCTGGAATGG	420
CAAATTCTGT CACATCTGTG TAGCACTTTT CCATTGTTTT AGAGCCTTCA AATTGGCCTT	480
GAATGAGATT CTCTGCCTTC TTACCAACGT CTCCTTTATG AGAAGATTTC GTTTCTGTCTG	540
CATTTTAGCT TGTAATTGA GTACTTTCAT CAAGCCTTGA ACTCTTTTAT GATTTACCAG	600
ATAAGCACGA TTCCTTAGTT CTAAATGAAT ACAGCGATAA GCATAATTTT CCTTGTGTTT	660
GATAAAAATG GATTGAATTT CAGCTTTAAG CTCTTGGTCC TTATCTGGTT TGTNTAG	717

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CTAAATCACC	AGATTTAACC	AAGTCGTAGA	TACGGCCTGG	TGTTCCAATA	ACAATATGAG	60
GCTGATTGCT	TGCCAATTTT	TCAATCTGGC	GAGCCTTATC	CGTACCACCC	ACATAATTAA	120
CCACACGAAC	TTCGACATCT	GAGTGAGCTG	AAATCTGACG	CGCTACTTGG	TAAATTTGAG	180
TAGCCAATC	ACGACTCGGT	GCAGTAATCA	CTGCTTGTAC	ACTATCGCTA	GCTTCATCTA	240
ATTGCTGGAA	AATCGGTAAC	AAGAAAGTAT	GAGTCTTACC	TGAACCTGTT	TTTGATTCTC	300
CTACTAGGTC	ACGACCTGCC	AAAACAATAG	GAATCAACTT	GTCTTGCACC	TCTGTTGGAG	360
TTGTAAATTT	TAACCTCTCC	AAGGCTTCTC	TAATATAGTT	TTTAAATTGA	AATTTTCGTAA	420
ATGACATAAC	ATCCTCGATT	CTATCTATCT	TATCAATTAT	ACCATATTTT	ATTCCATTAC	480
AGTAGTCTCA	CTTATTTAGG	CTATTTCCAG	TAGCTTCTCT	AGTAAGAAAA	GGCTGGAATT	540
TTATAGTTCC	AACCTCTTTT	CAGTTATTAT	TTCCAGTTTA	ACATAGCATT	CAAGCCATAG	600
TGATCACTCA	CTTGTGGACT	CTTGTTACCA	TCAAATACGA	CATGTAAATT	TTCCACCGCT	660
AACTCTTTGG	TAGTAAAGAC	ATAATCGATT	CGAAGGGGTT	CAGTGTTCCC	TTTCCAGCCA	720
TCAATTTTCA	GCGGAACAGT	ATAGCTACCA	CTTTTCTCTT	GAGCAACTTC	AAATGCGTCT	780
TGTAAGCCTA	ATGGACTAGC	TAAAATAGCT	TGGTAACCTT	CCCTGACCTG	CTGGGTTGTT	840
AAAATCTCCA	G					851

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTGTTGAGAT	TGTTACGAAA	TAAGTGAATA	TATTTAAGGA	GAAAATATAT	GTTGAAACAC	60
TTAAACTTAA	AAGGTCACCT	ATTGACAGCC	ATTTCCCTATA	TGATTCCAAT	TGTTTGTGGT	120
GCAGGATTCT	TAGTTGCCAT	TGGTTTAGCA	ATGGGGGGTG	GTGTTCTCTA	CGCTCTTGTA	180
GCAGGAAAAT	TCACTATCTG	GGATGCTTTA	GCAACTATGG	GTGGTAAAGC	CCTTGCTCTC	240

TTGCCAGTTG TTATTGCTAC AGGTTTGTCT TACTCGATTG CTGGTAAGCC AGGGATTGCA	300
CCAGGTTTTG TTGTTGGTCT AATTGCCAAT TCTGTTGGTT CAGGGTTTAT CGGTGGTATC	360
TTGGGAGGTT ATATAGTTGG TTTCTTGGTT CAAGCGATTA TTAAAAAGGT CAAAGTACCA	420
AACTGGATTA AAGGTTTAAT GCCAACCTTG ATTATTCCTT TTGTACCTCT TTGGTAAGTA	480
GTTTGATTAT GATTATATT ATTGGGGCGC CTATCGCAGC CTTTACCAAC TGGTTGACGA	540
G	541

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTGGAATGAG TGTATAAGCC CAGCCCAAGT TTTGCATCCG TTCAAAGTTC CAAGACCCTT	60
GTAAGAAGGT TGAACGCCAC CAAACTTTTT TACGATCTGA TTTAGTTAAT TGAAGTTTTT	120
CAGTCATGAT GTTTTCAGTC CTTTCTTATC TTAGTAGTCT TCTAGGATAT CGCCGATTGG	180
GTCGTTAGAA GTTGCGGCTC CTCCGCCACC ATTTCCACCA GTTTTAGAAA GGTGAAGGTA	240
GATAAGAGCG ATAGCAACAC CGATAGCACC GAATCCGATT AGAGTAATAT CTGACACAGC	300
AGCGAGAACG AAACCAAGAG CGAAGAATGG CCATACTTCA CGAGTTGCCA TCATGTTGAT	360
AACCATGGCG TAACCAACGG CAACGACCAT ACCACCACCG ATAGCCATAC CATCTTTGAG	420
CCAGTCTGGC ATGGCACTAA GGATACTTTG TACAGTTTCA GTTGGTACCA TAAGGAGAAG	480
AGCTGCAGGA AGCGCGATAC GAAGTCCTTG GAAAAGTAGC GCAATGAAAT GCGCACGCTC	540
CACAGCGCCG AAGTCACCTT TTTTAGCGGC AGCATCTGCA GTATGAACCA AACCACCTGA	600
AATTGTACGA ACAATCATTG TCAAGAAAAG TCCAGCTACG GCAAGAGGGA TAGCAACCGC	660
TTGGGCAACA CCGATACCAG TCTTGGTAAA GTCACCACCA AGAACCATGA TAATGGCAGC	720
AGCGACAGAA GCAAGTGCAG CATCAGGAGC GATAGCAGCA CCGATATTTG ACCAACCAAG	780
GGCAATCATT TGAAGCGATC CACCGAGGAT AATCCCTGCT TCCAAGTGGA CCTGTTACAA	840
GCCCAATAAG GGTACAGGCT ACAAGTGGTT GGTGAAATTG GAACTGGTCG AGGATGCCTT	900
CAAGACCTGC AAAGGAAGGC TACAACGACT ACTAAAACCA TAGAAATAAT AGACATGTTT	960
AAAATCCTTT CATAAATAAT GGCTTATTTG ACATTGGCTT TGTTAATCAA GTCAAACAAA	1020
TCTTTTTTAG AATCATTGTT TACTTTACGG ACATCAAATT CAACACCCAA GTCACGCATT	1080
TTTTCAAATG TAGCAACATC TTCTTTGTCC ATAGACAAAA CGGTATTGAC CAATGTTTTA	1140
CCTGTTGAGT GAGCCATAGA ACCAACGTTA AGAGTCTTGA TTGGCACGCC GCCTTCGATG	1200
GCACGAAGGG CATCTTGAGG TGTTTCAAAC AAGATAAGGG CATGTGTTTC TCCAAAACGT	1260
GGGTCTTTTG AAATATCAAT CAGTTTTTGA ATTGGAACCA CGTTAGCCTT GACATTACCT	1320
GGAG	1324

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

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TCATAAGGAA GCTGTCGCTC GTTCCGCTAA GGTATGGACA CCACGGTGAA CATTGGCATT      60
GTCCTGCTCA TAGTAAGTGT TAATAGCTTT CAGAACTACT AGTGGTTTTT GTGTCGTCGC      120
AGCATTGTCC AGATAGACCA GAGGTTTCATC ATTGACAATC TGATCTAAAA TTGGAAAATC      180
CTTGCGAATC GCTTCTACAT CTAACATAGG CTTCCCCTTA GCGTTTTGAC AATTTCCTCTT      240
CGATAGTTGC AATCATTTC AATCAGAACTT CCTTGACTGG AATCTCCACG ATAACAGATC      300
CAAGGAAACC ACGAACAACC AAACGCTCTG CAGTTGCCTT ATCCAATCCA CGACTCATGA      360
GGTAATACAT GTCTTCTGGA TCAACTTGTC CGATAGACGC TGCCTGTCCT GCAGTGACAT      420
CATTTTCATC AATCAAAAGA ATTGGGTTAG CATCTGAACG CGCTTGGTCT GAAAGCATGA      480
GAACACGGCT CTCTTGTTGC GCATCTGCTC CCTTAGCACC CTTGATGATG TGGCCGATAC      540
CATTGAAAGT CAAAGTTGCT TTTTCAAGGA TAACCCCATG TTGTAGGATA TTTCCGATAG      600
AGTTGCAGCC ATAGTTAGTT ACACGAGTAT CAATCCCTTG TACCTGACGA CCACTTGAAA      660
GAG

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(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 649 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

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CTAGTTGGAT GGCTTCAATA AAGGATGATT TGGCTGCTCC ACTATTGGCA ATGAGCTGAA      60
AACAGATATA TTCCATTTCT TCGTCATCTT ATTTCTCCTA TCCATTCAAG TGCTTGTTCC      120
AGAACTTTTG CTCCATTCAT CATTCCGTAA TCCCGCATAT CAATGGTATC TACAGGGATA      180
TTTCTTGCAA TTTCTTTTAC AGCAAGTAAC TCATAACGAA TTTGTGGCCC AATTAGAATG      240
ACATCTGCTT CATGGATATT CTTTTTAGCT TCTGTCATTG ATTTTGCTTG GATAGAAATT      300
TCAATCCCAC GTTCAGTCGC ACTTTGTTGC ATTTTTTTAA CAAGCATACT TGTCGACATT      360
CCCGCATTAC ATACTAATAA AATTTGTTTC ATAATCTTAA CCTTCCATTT CTTGTTCAAC      420
AACTTTGTCA TTAACCTTGA TAAATGGAAT GTATAGAAGA ACTCCAAGTG CAAAGATGAT      480

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GAATTGAACT AGAACTGCTC TCACGTCCCC TGCTGTTGCT AACCATGCAT TTAAGAATAC	540
TGGTGTAGTC CAAGGAACTT GTATAAATGC AGGACTCATG AATCCTGTAA CTGTTGCTAA	600
GTAGCTGATT AAAATACCAA GGACTGGAAC TGTGATAAAT GGAATAGTC	649

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTTGGTATTA TTTGAAATCA GATGGTTCTT ATGCAAAAAA TGCATGGCAA GGAGCTTATT	60
ACCTTAAATC AAACGGTAAA ATGGTACAAG GTGAGTGGGT TTATGATTCT TCTTACCAAG	120
CCATGGTATT ACTTGAAATC AGATGGTTCA TATGCTCGCA ATGCATGGCA AGGAAACTAC	180
TATTTGAAAT CAGATGGTAA AATGGCTGTC AATGAATGGG TTTATGATGC CACCTATCAA	240
GCATGGTATT ATTTGACATC AGATGGTTCT TATGCTTACA GTACATGGCA AGGAAATTAC	300
TATCCTAAAA TCGGATGGTA AAATGGCTGT CAATGAATGG GTTGATGGTG GACGTTATTA	360
TGTTGGCGCT GACGGAGTTT GGAAGGAAGG TCAAGCAAGT ACAGCTTCTC CTAGTAATGA	420
TAGCAATAGT GAATATTCCT GCTGCTTTAG GAAAGGCAAA AAGTTATAAT TCGTTATTCC	480
ACATGTCAAA AAAAACG	497

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTAGTCTAAA TTTTAAATAA CAAAGGTCAA AGATAGTCAA TATCAGTAAT CATAACTAAG	60
TAAACAAAAA GAGGTAAAGA ATATGAATAA CAACTTTAAT AATTTTAATA ACATGGATGA	120
TTTATTTAAC CAATTGATGG GTGGTATGCG AGGATACAGT TCTGAAAATC GCCGTTACTT	180
AATTAATGGA CGCGAAGTCA CACCTGAGGA ATTTGCTCAC TATCGTACGA CTGGTCAATT	240
ACCAGGAAAT GCAGAACTG ATGTGCAAAAT GCCACAACAG GCATCAGGTA TGAAACAAGA	300
CGGTGTCCTT GCAAACTAG GTCGAAACTT GACAGCAGAA GCGCGTGAGG GCAAGTTGGA	360

TCCTGTTATC	GGACGAAACA	AGGAAATTCA	AGAAACATCT	GAAATCCTCT	CACGCCGCAC	420
CAAGAACAAT	CCTGTTTTGG	TCGGAGATGC	AGGTGTTGGT	AAGACAGCAG	TTGTCTGAAG	480
TCTAGCGCAA	GCCATTGTGA	ACGGAGATGT	TCCTGCTGCT	ATCAAGAACA	AGGAAATTAT	540
TTCTATTGAT	ATCTCAGGTC	TTGAGGCTGG	TACTCAATAC	CGTGGTAGCT	TTGAAGAAAA	600
TGTCCAAAAC	TTAGTCAATG	AAGTGAAAGA	AGCAGGGAAT	ATTATCCTCT	TCTTTGATGA	660
AATTCAACAA	ATTCTTGGTG	CTGGTAGCAC	TTGTGGAGAC	AGTGGTTCTA	AAGGGCTTGC	720
GGATATTCTC	AGCCAATCGA	TCTCTCTCGT	GGAGAATTGA	CAGTGATTGG	GGCAACAAC	780
CAAGACGAAT	ACCGTAACAC	CATCTTGAA	AATGCTGCTC	TTGCTCGTCG	TTTCAACGAA	840
GTGAAGGTCA	ATGCTCCTTC	AGCAGAGAAT	ACTTTTAAAA	TTCTTCAAGG	CATTCTGTGAC	900
CTCTATCAAC	AACACCACAA	TGTCATCTTG	CCAGACGAAG	TCTTGAAAGC	AGCGGTGGAT	960
TATTCTGTTT	AATACATTCC	TCAACGTAGC	TTGCCAGATA	AGGCTATTGA	CCTTGTTCGAT	1020
GTAACGGCTG	CTCACTTGGC	GGCTCAACAT	CCAGTAACAG	ATGTGCATGC	TGTTGAACGA	1080
GAAATCGAAA	CGGAAAAAGA	CAAGCAAGAA	AAAGCAGTTG	AAGCAGAAGA	TTTTGAAGCA	1140
GCTCTAAACT	ATAAAACACG	CATTGCAGAA	TTGGAAAGGA	AAATCGAAAA	CCACACAGAA	1200
GATATGAAAG	TGACTGCAAG	TGTCAACGAT	GTGGCTGAAT	CTGTGGAACG	AATGACAGGT	1260
ATCCCAGTAT	CGCAAATGGG	AG				1282

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTTGATATAA	TTCTTGTTTC	GAAAGATTCT	CCTTAGGTAT	ATCTATTCCT	CCACTAGTAA	60
ACGGTAATTC	CAAAACAGAG	TTTACTTCGT	TAAATGTAAG	CCAATATTTA	ACTTTATCTT	120
TATACCTTTC	TAAAACTGTT	CGAGCAAATT	TTTCATAAAA	ATGAATCATT	CTTCCTATCA	180
ATCCATCCAT	GATATTTTCT	TGCTAAATAT	AATGGAGTCT	CATAGTGTGA	AAGAGTTACA	240
AGTGGTTCTA	TCCCGTGAGC	ATGTAGTTCA	TCAAACAATT	CATCATAATA	TTTCAATCCA	300
GCTTCGTTAG	GTTCTTCCTC	ATCTCCTTTT	GGAAAAATTC	TACTCCATGC	AATAGAAGTA	360
CGAAAAACAT	TAAAGCCCAT	TTCAGAAAAC	AAGGATATAT	CTTCCTTATA	TTTATGATAA	420
AAATCAATAC	CTATCAATTT	TAAGTTATCT	TCTGTAGGAT	TTTCTGTTGC	TTCTCCTAAT	480
CCACCTTTGG	GTAACACATC	CTGAAGTAT	AAGCCCTTAC	CATCTTCATT	ATATGCTCCC	540
TCTACTTGAT	TAGCTGCAAC	AGCTCCACCC	CAAAGAAAAT	CATCTGGAAA	AATGGTCATA	600
ACTTTCCTCC	ATTATAATAT	TACCAGTAAT	TCCTTAGAAA	TGCTCGATTG	TCTGATTATT	660
AGGTAATATT	AATACATCTA	GAAAATCATT	GGTATTCGTT	ACAATTACTG	GTGTAAGTGT	720
TTCGTAGCCT	TTAGTCTTGA	TTAAATTCAA	GTCCATTTCA	AAAATCAACT	GATTTTTTGAA	780
AACTCTGTCT	CCTTCTTCTA	CATGACTAAT	AAAACCTTGA	CCTTTTAG		828

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AGCTATGGTC	AGACTCAGAT	TGATGGCGTT	GCTTATGCCA	AGTACGATAT	CTTCCGTTTA	60
AAGAACGGGA	AAATTGTGGA	GCATTGGGAT	AATAAGGAAG	TCATGCCTAA	GGTAGAAGAC	120
TTGACCAATC	GAGGGAAGTT	TTAAATTGAG	GACAAAGAAT	GATTGAATAC	AAAAATGTAG	180
CACTGCGCTA	CACAGAAAAG	GATGTCTTGA	GAGATGTCAA	CTTACAGATT	GAGGATGGGG	240
AATTTATGGT	TTTAGTAGGG	CCTTCTGGGT	CAGGTAAGAC	GACCATGCTC	AAGATGATTA	300
ACCGTCTTTT	GGAACCAACT	GATGGAAATA	TTTATATGGA	TGGGAAGCGC	ATCAAAGACT	360
ATGATGAGCG	TGAACCTTCG	CTTTCTACTG	GTTATGTTTT	ACAGGCTATT	GCTCTTTTTT	420
CAAATCTAAC	AGTTGCGGAA	AATATTGCTC	TCATTCCTGA	AATGAAGGGG	TGGAGCAAGG	480
AAGAAATTAC	GAAGAAAACA	GAAGAACTTT	TGGCTAAGGT	TGGTTTACCA	GTAGCCGAGT	540
ATGGGCATCG	CTTACCTAGT	GAATTATCTG	GTGGAGAACA	GCAACGGGTC	GGTATTGTCC	600
GAGCTATGAT	TGCTCAGCCC	AAGATTTTCC	TCATGGATGA	ACCCTTTTCG	GCCTTGGATG	660
CTATTTTCGAG	AAAACAGTTG	CAGGTTCTGA	CAAAAGAATT	GCATAAGAG	TTTGGGATGA	720
CAACGATTTT	TGTAACCCAT	GATACGGATG	AAGCCTTGAA	GTTGGCGGAC	CGTATTGCTG	780
TCTTGCAGGA	TGGAGAAATT	CGCCAGGTAG	CGAATCCCCG	GACAATTTTA	AAAGTGCCTG	840
CAACAGACTT	TGTAGCAGAC	TTGTTTGGAG	GTAGTGTTCA	TGACTAATTT	AATTGCAACT	900
TTTCAGGATC	GTTTATAGTA	TTGGTTGACA	GCTACAATGA	CATTGGTCGG	TTCTTTGAGC	960
AAGAGATAGA	TTAGCCAGAC	AGTCATGCCC	AAAATCCCTC	CAGGTAAGAG	CATAGACCGT	1020
TGCACATTAA	GTACGATTAA	AAAAGTGATA	ATGGCAAGAA	AACTTGCTAC	TGCTTGTAAT	1080
AAAAAGGTTG	TTAGTGTCAT	ATTAGTTCAT	CAATACCAAG	GCGACAGAAG	TTCTTGCCCC	1140
TAAAGCGAGG	GTAATGAGCA	GGGATTCAAA	CATCTTACTC	ATACCAGAGT	TTATGTGGTT	1200
GGTCATAATA	TCACGGACCG	CATTGGTCAA	GGCAATACCT	GGTACAAACG	GCATGACCGC	1260
ACCAGCTATA	ATCAAATCCT	GCCCGTTTGA	ATGGAAAAAC	CCTGTGTTAG	CCGAGCCCCA	1320
AAACTGGGGC	CAATTTATCC	CCCAAAGACA	AAAGCTCCAT	CAAAGGCTGT	CACAAAGGGA	1380
ATTCGGATAA	ATTTTCCACA	TAGAAGGAAA	AGGCAAAACC	AAATAAGGTC	GCCACTCCTG	1440
CCCCAAGTGC	TCGTAAATAT	TCCGCT				1466

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AAGGTTCTTC GTAAATGTAC ACCATTCGGA TGCTCAAAAT GGGTTCTGAA GCTGCTGCTA	60
AATCTGCACA AGAACACGGT CTAAATCAG TTGAAGTTAC TGTAAGAGGT CCAGGTTCTG	120
GTCGTGAGTC AGCTATTTTCG TGCCTTGCT GCCGCTGGTC TTGAAGTAAC AGCAATTCGT	180
GATGGGACTC CAGTGCCAAC ACAATGGTGC TTCGTCTCC AAAACGTCGC CGTGATAAT	240
CATCGCATT CACTGCTTTT CGTTTAAGAG GGAGTAACTA AATGATCGAG TTTGAAAAAC	300
CAAAATATAAC AAAAATTGAT GAAAATAAG ATTATGGCAA GTTAGTAATC GAACCACTTG	360
AACGTGGCTA CGGTACAGCT CTTGGTAACT CTCTTCGTCG TGTACTTCTA GCTTCTCTAC	420
CAGGAGCAGC TGTGACATCT ATCAACATTG ATGGTGTGTT ACATGAGTTT GACACAGTTC	480
CAGGTGTTTCG TGAAGACGTG ATGCAAAATCA TTCTGAACAT TAAAGGAATT GCAGTGAAAT	540
CGTACGTTGA AGACGAAAAA ATCATCGAAC TGGATGTTGA AGGTCCTGCT GAAGTAACAG	600
CTGGTGACAT TTTGACAGAT AGCGATATTG AAATTGTAAA TCCAGATCAT TATCTCTTTA	660
CAATTGGTGA AGGTTCTTCT CTAAAAGCGA CTATGACTGT TAACAGTGGT CGTGGATATG	720
TACCTGCTGA TGAAAATAAA AAGGATAATG CACCAGTTGG AACACTTGCT GTAGATTCTA	780
TTTATACACC AGTTACAAAA GTCAACTATC AAGTGGAACC TGCTCGTGTA GGTAGCAATG	840
ATGGTTTCGA CAAATTAACC CTTGAAATCT TGACAAATGG AACAATTATT CCAGAAGATG	900
CTTTAGGGCT TTCAGCACGT ATTTTGACAG AACATCTTGA TTTGTTTACA AATCTTACTG	960
AGATTGCTAA GTCAACTGAA GTGATGAAAG AAGCTGATAC TGAATCTGAC GACCGTATTT	1020
TAGATCGTAC GATTGAGGAA CTGGACTTGT CTGTGCGTTC ATACAACTGT TTAACACGTG	1080
CCGGTATCAA TACTGTGCAT GATTGACAG AAAAATCTGA AGCAGAGATG ATGAAAGTAC	1140
GAAATCTTGG ACGCAAGAGT TTGGAAGAAG TGAAACTCAA ACTCATTGAT TTGGGTCTTG	1200
GATTAAAAGA TAAATAAAGG AGGAATACAT GGCTTACCGT AACTAGGAC GCACTAG	1257

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1332 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single.

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTATTGAAAC AAGAAAAATA GAGAATCAAA GAAAGAGAAC TTATGAATAT TCAAGAAGAA	60
ATTAAGAAAC GTCGTACCTT TGCCATTATC TCCCACCCGG ACGCGGGGAA AACAACCATC	120
ACTGAGCAGT TACTCTAACT TTGGGGGTGA GATTCTGTGAG GCTGGTACGG TAAAAGGGAA	180
GAAAACAGGG ACTTTTGCTA AATCTGACTG GATGGATATC GAGAAGCAAC GTGGGATTTC	240

TGTTACTTCA	TCTGTTATGC	AATTTGACTA	CGACGGCAAG	CGCGTGAATA	TCTTAGACAC	300
GCCAGGGCAC	GAGGACTTCT	CAGAAGATAC	CTATCGTACC	TTGATGGCGG	TGGATGCTGC	360
GGTCATGGTC	GTGGACTCTG	CCAAGGGGAT	CGAGGCTCAA	ACAAAGAAAT	TGTTTGAGGT	420
TGTGAAACAT	CGTGGCATTG	CAGTCTTTAC	CTTTATGAAC	AAGTTGGATC	GTGACGGTCG	480
TGAGCCTTTG	GATCTCTTGC	AAGAATTGGA	AGAAATCTTG	GGCATTGCTA	GCTACCCTAT	540
GAAGTGGCCT	ATCGGGATGG	GGAAAGCCTT	TGAGGGCTTG	TATGACCTCT	ATAACCAACG	600
TTTAGAGCTT	TACAAAGGGG	ATGAGCGTTT	TGCTAGCCCT	AGAAGATGGA	GACAAACTTT	660
TTGGTAGCAA	TCCTTTCTAC	GAGCAAGTCA	AGGATGACAT	TGAGCTTTTA	AATGAAGCTG	720
GGAATGAGTT	TTCAGAGGAA	GCTATTCTGG	CTGGAGAATT	GACGCCTGTC	TTTTTCGGTT	780
CAGCCCTGAC	AACTTTGGT	GTGCAGACCT	TCCTTGAAAT	CTTCCTCAAG	TTTGCTCCAG	840
AACCACATGG	TCACAAGAAA	ACAGACGGTG	AAATTGTGGA	TCCTTATGAC	AAGGATTTCT	900
CAGGCTTTGT	CTTTAAAATC	CAAGCCAACA	TGGATCCTCG	TCACCGTGAC	CGTATTGCCT	960
TTGTCCGTAT	CGTATCAGGC	GAATTTGAGC	GTGGCATGAG	TGTCAATCTC	CCTCGTACTG	1020
GTAAGGGTGC	CAAATATCT	AATGTTACCC	AGTTTATGGC	GGAGAGTCGT	GAGAATGTGA	1080
CCAATGCCGT	AGCAGGTGAT	ATTATCGGGG	TTTACGATAC	CGGTACTTAT	CAGGTTGGGG	1140
ATACCTTGAC	GGTTGGAAAA	AACAAGTTTG	AATTTGAACC	ACTGCCAACC	TTTACTCCTG	1200
AAATTTTCAT	GAAAGTTTCT	GCTAAGAATG	TTATGAAGCA	AAAATCCTTC	CACAAGGGGA	1260
TTGAGCAATT	GGTGCAAGAA	GGAGCCGTTC	AGCTTTATAA	GAATTACCAA	ACAGGTGAGT	1320
ACATGCTGGG	AG					1332

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 932 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TTGGACGCTG	GAACAAATCC	AAGCTGACCT	GTTCCAAGAC	CAGACTTGGT	ATGCTCTGGC	60
TTATGATGGG	GCAGAAGTGA	TTGGCTTTCT	AGCTGTTTCT	GAGACTCTTC	TTTGAAGCAG	120
AAGTCCTGCA	AATCGCTGTC	AAAGGAGCCT	ATCAGGGTAA	GGGCATTGCG	TCAGCCTTGT	180
TTGCTCAATT	GCCGACAGAC	AAGGAAATTT	TCCTCGAAGT	CAGACAGTCA	AATCAACGAG	240
CGCAAGCATT	TTACAAGAAA	GAAAAGATGG	CAGTTATCGC	TGAGCGAAAG	GCCTACTACC	300
ATGACCCAGT	CGAGGACGCC	ATTATCATGA	AGAGAGAAAT	AGATGAAGGA	TAGATATATT	360
TTAGCATTTG	AGACATCCTG	TGATGAGACC	AGTGTGCGCG	TCTTGAAAAA	CGACGATGAG	420
CTCTTGTTCA	ATGTCATTGC	TAGTCAAATT	GAGAGTCACA	AACGTTTTTG	TGGCGTAGTG	480
CCCGAAGTAG	CCAGTCGTCA	CCATGTGCGAG	GTCATTACAG	CCTGTATCGA	GGAGGCATTG	540
GCAGAAGCAG	GGATTACCGA	AGAGGACGTG	ACAGCTGTTG	CGGTTACCTA	CGGACCAGGC	600
TTGGTCGGAG	CCTTGCTAGT	TGGTTTGTC	GCCGCCAAGG	CCTTTGCTTG	GGCTCACGGA	660
CTTCCACTGA	TTCTGTGTTA	TCACATGGCT	GGGCACCTCA	TGGCAGCTCA	GAGTGTGGAG	720

CCTTTGGAGT	TTCCCTTGCT	AGCCCTTTTA	GTCAGTGGTG	GGCACACAGA	GTTGGTCTAT	780
GTTTCTGAGG	CTGGCGATTA	CAAGATTGTT	GGAGAGACAC	GAGACGATGC	AGTTGGGGAG	840
GCTTATGACA	AGGTCGGTCG	TGTCATGGGC	TTGACCTATC	CTGCAGGTCTG	TGAGATTGAC	900
GAGCTGGCTC	NTCTNNGGCA	GGANATTTAT	GA			932

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTAAACTTTC	GCTCATAGGC	ATACAAATTA	ATCCTTTGGC	ATAAGTAGCC	ATAAAATTAA	60
CATTTTCTGT	TGTAGCTGCT	TGTGCAGAAC	AAATTAAGTC	TCCTTCATTT	TCTCTATCCT	120
TGTCGTCTAT	AACAAGAACA	AGTCGTCCCT	TCTGCAATGC	TTCTAATGCT	TCTTGTATTT	180
TTTCGATATTC	CATTGACTGA	TTATCCTTTC	TGCTAAAATC	CATTTTGATA	TAATAGTTCC	240
TTTCGATATTT	CTGATTTTGG	AGAGTTATCC	ATCAGTTTTT	GCACATATTT	ACCTAAGATA	300
TCATTTTCAA	GATTTACTGT	ACTCCCGACT	TGTTTTACTCT	TAAGAATGGT	TTGTTTCAAG	360
GTATGAGGGA	TAACAGATAC	TGAAAAGTTT	ACTTTGGAGA	CTTTAGCGAC	AGTCAGACTA	420
ATGCCGTCAA	TTGTAATAGA	TCCTTTTTCA	ACTATTAAAT	CTAAAATTTT	TTTTTGTGTG	480
TTGATTTGAT	ACCATACAGC	ATTATCATCT	TTTTTTTATTG	ACGAGATTTT	TCCTGTACCA	540
TCAATGTGTC	CTGTAACGAC	GTGACCCCCA	AGTCGACCGT	TGACAGATAA	GGCTCTTTCT	600
AGATTCACCT	CACTTCCATG	TTTAAATAGA	GTAAGAGCTG	TTCGACTCCA	TGTTTCATTC	660
ATTACATCAA	CTGTAAAGGA	TTGATGATTG	AAATGAGTAA	CTGTAAGACA	GATACCATTT	720
ACTGCTATAC	TATCGCCTAA	ATGGATATCC	GTAAATATTT	TTGAGGCTTT	AATTGATAGT	780
TTACAATTAC	GAGAGTCTTT	CTGTATTCCT	TCAACTTTTC	CGATTTCTTC	AATTATTCCT	840
GTGAACATGG	ATAAATCACT	TCACTTTCTA	TGAGATAGTC	NTTCCCTNTT	TGAGAAAAAG	900
CATAAGGTTT	CAATCTAATA	GCGTCATTG	GCAAAGAAAT	GCCTTCACCT	CCGACAGGAA	960
ACTTGGCACT	GCCTCCAAAA	ATTTTGGTG	CAATATATAT	TTTCAGCTCA	TCAACAATTT	1020
GTTGTTCCAA	AGCACTCCAA	TTCATTAGAC	TGCCCCCCTC	TACAACTAGG	CTATCAATCT	1080
GCATGTTTCC	TTAGATGTTN	GCATTAAACT	CNGATAAGTC	TATATGATTG	CCTTTTTTCT	1140
TTATGGAAAG	TATCCCCC					1158

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

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TAAAGGCTGT TTGGATAATG TAACATAAAG AAATCTTGTT TAGCAGGGAT TGAATAGAGT      60
TCCTGAAGTG ATGACTTCTT TATTAGACAT AATGTCTGGA CCCAAGATTA AAAGAATGGC      120
CCCGAAGAAT ACGAGCATCA AAGGTAGCAG ATGCAACAAC TGTATCGTGG AAGATTGAGA      180
GGAACCTTAG TAATTTAAGA TTGTCTAAAC TTTCTTCTTT CTTACCAAAG CGTCCTGCTA      240
CTTTATCTAC AAACCAGATT GCAAATTGCT GTTGGTGACC AATCGCAAAT CCGCCACCAC      300
CAGTCAAGCG TTGAGTTGCC TCAACAGTCA TATTTGAACT AACTGCCCAG TAAAGTCCAC      360
AGATGATACC AATCGCTGCT GTACCGTAAG CATTGCGCAA TTGTGGTACT AAGAATAGAA      420
CCATAAGAGA TACTGTTGCA GCTAGCCATG CTGATCAATT CCCTCAACCA GTCCTATATC      480
TCAGCCAAGA GAATCGAGGA GGTCTTTGCG GAATCTCCCG AAAACATCCA TTCAGAATTA      540
GAACAAAAGC AAGTTACCAG TGGTCGGGTT TTACAAGTCC AAGAATTGAC TTTTACCTAT      600
CCTGATGCGG CCCAGCCTTC TCTGAGAGAC ATTTCTTTTG ATATGACTCA AGGACAAATC      660
CTTGGTATCA TTGGGGGGAC TGGTTCTGGT AAATCAAGCT TGGTGCAACT CTTACTTGGA      720
CTTTATCCAG TAGACAAGGG GAACATTGAC CTTTATCAAA ATGGACGTAG TCCTCTTAAT      780
TTGGAGCAGT GCGGTCTTG GATTGCCTAT GTACCTCAA AGGTCAAAC CTTTAAGGGA      840
ACTATTCGTT CCAACTTGAC TTTAGGTTTA AATCAAGAAG TATCTGACCA GAAACTCTGG      900
CAGGCCTTGG AGATTGCGCA AGCTAAGGAT TTTGTCACTG AAAAGGAAGG ACTTTTGGAT      960
GCCCTAATTG AAGCAGGGGG GCGAAATTTT TCAGGTGGAC AAAAACAAAG GTTGTCTATC     1020
GCCCAGACAG TCTTGCGCCA AGCTCCGTTT ATCATCCTAG ATGATGCAAC CTCGGCACTG     1080
GATACCATTA CAGAGTCCAA GCTCTGAAA GCTATTAGAG AAAATTTTCC AAACACGAGC     1140
TTAATTTTGA TCTCTCAACG AACCTCAACT TTACAGATGG CGGACCAGAT TCTCCTCTTG     1200
GAAAAAGGTG AGTTGCTAGC TGTTGGCAAG CACGATGACT TGATGAAATC CAGCCAAGTC     1260
TATCGTGAAA TCAATGCATC CCAACATGGA AAGGAGGACT AGAATGAAAC GACAAACTGT     1320
AAACCAGACG CTCAAACGTT TAGCCGTAGA TTTAGCAAAC CATCCCTTCC TCCTTTTCCT     1380
AGCCTTTCTA GGAACCTATT CCCAAGTTGG CTTATCAATT TACCTACCTA TTCTGATTGG     1440
GCAGGTCATT GACCAAGTCC TAGTGGCTGG TTCATCACCA GT                          1482

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(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 895 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTCTGAAGGA	TCCAGAAAGT	CGCTTATATA	TTTTATTAAA	AGACGGTCAG	GTTATTGGGA	60
CTTGTACGGT	TGATTTATCG	ACTAATACGA	ATTACTTCTA	CGGTTTAGCA	ATATTGGAAC	120
CTGAACGTGG	AAAAGGCTAT	GGAAGCTACT	TAGCAAAATC	CCTCGTCAAC	CAACTAATTG	180
AGCAAAATGA	CAAGGAATTT	CAGATTGCAG	TGGAAGATAG	CAATGTAGGT	GCCAAACGTT	240
TGTATGAAAA	AATTGGCTTT	GTCAAACAGA	CTCAGGTGGT	TTATCTGAAT	GAGAAAGGAG	300
CAAGGGATTG	CGAAGTGTAG	AGATATTCGG	ACTGAAATTT	ACTTGAACCTT	TTAGTGATGA	360
AACTAATTGT	TCTTGGATTT	CAGCTTTCCT	GATTATGATT	TATGATTAAA	ATCTATGACA	420
CCATGTCTCG	TGATTTGCGA	GAATTTGTCC	CGATTGAGGA	CGGCAAGATC	AAGATGTATG	480
TTTGTGGGCC	AACGGTGTAC	AACTATATCC	ACGTGGGAAA	CGCCCGTTTCG	ACGGTAGCTT	540
TTTTGGATAC	GAATTTCTGC	GCTATTTTGA	GTACCGTGGG	TATAAGGTTG	CCTATATTTT	600
CAATTTTACA	GATGTGGATG	ATAAGATTAT	CAACCGTGCC	AGGGAAGAAG	GCATCACGCC	660
TCAGGAGGTT	GCGGATAAGT	ACATCGCTGC	CTTTCGTGAG	GATGTGACGG	CCTTGGGCGT	720
GAAACCTGCG	ACTCGCCATC	CGCGTGTAGT	GGAGTTTATG	GCAGACATCA	TCCGTTTGTG	780
GGAAGACTTG	ATCGAGAAAG	GCTTTGCCTA	TGAGAGTCAA	GGGGATGTCT	ATTTCCGTGT	840
AGAAAAATCC	CACAACTATG	CTAAATTGGC	TAATAAAACC	TTGGAAGATT	TGGAG	895

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTGTTTGCCC	TTTCTTCTAA	TAAAGAATTG	GCAGAACGTG	TGGCGCAGGA	GATTGGGATA	60
GAGTTGGGGA	AATCAAGTGT	TCGCCAATTT	TCAGATGGAG	AGATTCAGGT	CAACATTGAA	120
GAATCAATCC	GTGGGAAACA	CGTCTTTATC	CTACAATCAA	CTAGTTCGCC	TGTAAATGAC	180
AATCTGCTTG	AAATTTTGAT	TATGGTAGAT	GCTTTGAAGC	GTGCGAGTGC	AGAATCTGTC	240
AATGTTGTCA	TGCCTTACTA	TGGGTATGCA	CGTCAGGATA	GAAAGGCGAG	AGCGCGTGAG	300
CCAATCACTT	CAAACTTGT	CGCAAATATG	CTTGAAGTAG	CTGGAGTGGA	TCGTTTATTG	360
ACCATCGACT	TGCATGCTGC	GCAAATTCAA	GGATTCCTTG	ATATTCCTGT	GGATCATTTG	420
ATGGGTGCTC	CTCTGATTGC	AGATTATTTT	GAGCGTCCTG	GTATGGTTGG	TTCTGACTAT	480
GTGGTTGTCA	GCCCGGACCA	TGGAGGGGTG	ACTCGTGCTC	GTAAGTTGGC	AGAATTTTTG	540
AAAACATCTA	TCGCTATTAT	TGAGAAACGT	CGTAGCGTTG	ATAAGATGAA	TACTAGTGAA	600
GTTATGAACA	CCATCGGTAA	GGTTGAAGGC	AACCACTTGT	AGCTTCGATT	GATGATATGT	660
ATTGATACCG	CTGGAACGAT	TTGTCATGCG	GCAGATGCTC	TTGCGGAAG		709

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CTAGAAGAAC	TCCGTCACAA	GCTTGTGACT	TGTAAGCAAG	AACAGAGCAA	GATTGAGGAT	60
TCCTTATGAT	TTCATTCTT	CTTCTATTGG	TCTTGGTTTG	GGGATTTTAT	ATCGGCTATC	120
GGAGAGGCCT	GCTCTTACAG	GTTTATTACC	TGATTTCAGC	CATGGCATCG	GCTTTTATGG	180
CTGGCCAGTT	TTATAAGGGG	CTTGGAGAGC	AATTCCATTT	ATTGCTCCCT	TATGCAAATT	240
CGCAGGAAGG	TCAGGGGACT	TTCTTTTTC	CATCGGATCA	ACTCTTTCAG	CTGGATAAGG	300
TCTTTTATGC	AGGTATCGGC	TACTTGCTTG	TATTTGGGAT	TGTCTATAGC	ATTGGTCGTT	360
TGCTTGGTCT	TCTCTTACAC	TTGATTCTTA	GCAAAAACT	GGGTGGTAAG	TTGTTCCAAG	420
TTTCAGCAGG	TATCTTGTCC	ATGTTGGTGA	CCTTATTTGT	CTTGCAAATG	GCCTTGACAA	480
TCTTGCGCAC	CATCCCCATG	GCAGTTATAC	AAAATCCTCT	TGAAAAGAGT	ATCGTCGCAA	540
AACACATCAT	CCAGAGCATA	CCGATAACAA	CCAGTTGGCT	CAAACAAATC	TGGGTGACAA	600
ATTTAATCGG	ATAAAAAGGG	CAGGAGTTTT	CCTAGCCCTT	TGTTTACAGA	TTGACTCGA	660
ATCTATCAGA	ATGTAAAAAG	CTACCACACC	TAGACATTCA	AAGACAAGGA	AATAAAGATG	720
AATAAGAAAA	TATTAGAAAC	ATTAGAGTTC	GATAAGGTCA	AGGCCTTGTT	TGAGCCTCAT	780
TTGTTGACCG	AGCAGGGCTT	GGAGCAATTG	AGACAG			816

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1001 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CTTGAAGCAG	CTGAAAGCAT	GGGGTCTTCG	GGATTTAAAA	CCTATTCGTA	ACGGGTGTGT	60
TTACCTTTCC	TAGTTCCAAC	CTTACTAGCA	GCTCCTTGCT	TGTATTTATG	AGAGCATTCT	120
CAGACTTTGG	AACGCCTATG	TTGATTGGCG	AAGGATATCG	GACTTTCCCT	GTCTGTATTT	180
ATACCCAATT	TATTAGCGAG	GTTGGAGGAA	ATTCTGCTTT	TGCAATTATG	GCGATTATCA	240
TTGCCTTGGC	AATTTTCCTT	ATCCAAAAAC	ACATTGCAAA	CCGCTACAGT	TTCAGCATGA	300
ATCTGCTCCA	TCCAATTGAG	CCTAAAAAAA	CTACAAAAGG	AAAAATGGCT	GCCATTTATG	360
CAACAGTCTA	CGGAATTATC	TTTATCTCTG	TTTACCTCA	AATCTACTTA	ATTTATACCT	420
CTTTCCTAAA	AACATCAGGT	ATGGTATTTG	TTAAAGGTTA	TTCTCCAAAC	AGTTACAAGG	480

TAGCTTTCAA	TCGTATGGGA	TCTGCTATTT	TCAATACCAT	TCGTATCCCT	TTGATTGCCT	540
TAGTTCTAGT	TGTTCCCTATT	TACGACATTT	ATCTCCTACC	TAGCCGTTAG	AAAACGGAAT	600
TTGTTTACAA	ACTTAATTGA	CAGCCTCAGT	ATGGTACCTT	ATATTGTACC	AGGAACCGTT	660
CTAGGGATTG	CCTTCATTTT	TTCTTCAAT	ACTGGTCTAT	TTGGAAGTGG	ATTTCTTATG	720
ATTACAGGGA	CTGCTTTTCAT	CTTGATTATG	TCTCTATCTG	TCAGAAGATT	ACCGTATACT	780
ATTCGCTCAT	CTGTTGCTAG	CTTACAACAA	ATAGCACCAA	GTATTGAAGA	AGCTGCTGGA	840
AAGCTTAGGA	AGTAGTCGTC	TCAATACCTT	TGCTAAGATT	ACAACTCCAA	TGATGCTATC	900
TGGTATCATT	TCTGGAGCCA	TCTTATCTTG	GGTCACAATG	ATTTCAAAAC	TCTCTACTTC	960
TATCCTCCTC	TACAATGTCA	AAACAAGAAC	AATGACTGTA	G		1001

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1064 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CTGGTTTGCA	ATCTATTCCA	ACTGAGATTA	CAGAGGCAGC	AAGGATTGAT	GGTGCGACTA	60
GCAAGCAAGT	TTTCTGGAAC	ATTGAATTGC	CTTACTTGCT	ACCAAGTGTC	TCTATGGTCT	120
TTATCCTAGC	CCTAAAAGGT	GGGCTGACTG	CCTTTGACCA	AGTCTTTGCC	ATGACCGGTG	180
GTGGTCCAAA	CAATGCCACA	ACCTCACTTG	GGCTCTGGT	TTATAACTAT	GCCTTTAAAA	240
ACAACCAATT	CGGTTATGCC	AATGCCATTG	CCGTAATCTT	GTTCTCTTA	ATTGTAGTGA	300
TTTCGATCAT	CCAATTGAGA	GTATCTAAGA	AATTTGAAAT	TTAAGAGGAG	AAGCATGATG	360
AAACAAGATG	AAAGAAAAGC	CCTGATTGGC	AAATACATTC	TATTGATTCT	AGGATCGGTT	420
CTGATTTTAG	TGCCGCTCCT	TGCTACCCTC	TTAGTTCCT	TTAAACCCAC	TAAGGATATT	480
GTAGATAATT	TCTTTGGCTT	TCCAACCAAC	TTACATGGG	ACAACTTTAG	CCGTCCTTA	540
GCTGATGGGA	TTGGAGGCTA	TTATTGGACT	CTGTCGTCAT	CACTGTCTTG	TCTTTACTTG	600
CAGTAATGAT	CTTTATCCCT	ATGGCAGCCT	ACTCCATCGC	TCGCAATATG	AGTAAAAGAA	660
AAGCCTTTAC	CATTCATGTA	TACCCTCTTA	ATCCTCGGAA	TCTTCGTACC	TTTCCAAGTC	720
ATCATGATTC	CGATTACGGT	TATGATGAGT	AAACTCGGTT	TGGCTAATAC	CTTTGGTTTG	780
ATCTTGCTCT	ACTTGACCTA	TGCGATTCCA	CAGACCCTCT	TTCTCTATGT	TGGATATATC	840
AAAATCTCGA	TTCCAGAAAG	TCTGGATGAA	GCAGCAGAGA	TCGATGGGGC	TAATCAATTT	900
ACAACCTATT	TCCGCATCAT	NTTCCCAATG	ATGAAACCGA	TGCATGCGAC	AACCATGATC	960
ATCAATGCCC	TTTGGTTCTG	GAATGACTTC	ATGTTGCCAC	TCCTTGCTCT	GAACCGGGAT	1020
TCCAAAATGT	GGACTCTGCC	TTTGTTCCTA	TACAACTACG	CAGG		1064

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CTGTAAAAGA AGTTAATCAA GTTGATAAAG CACTTTTAAA ACAAATTGGT GCAGTTGATG	60
TCTTAGAAGT GAAGGGTGGC ATTCAAGCAA TCTATGGAGC AAAAGCAATC TTATATAAAA	120
ATAGTATTAA TGAAATTTTA GGTGTAGATG ATTAAGTACT TACTGACTTA ATAAAAACA	180
GAGGAGAGTG ATGGATGAGT AGGATGAAAT GAAATCGCAT ACAAGAAATA AAGAACTCAT	240
TATCCAAGTT GGATACGCTT ATTACATAGG AGAATACAAA TGAAATTTAG AAAATTAGCT	300
TGTACAGTAC TTGCGGGTGC TCGGTTCTT GGTCTTGCTG CTTGTGGCAA TTCTGGCGGA	360
AGTAAAGATG CTGCCAAATC AGGTGGTGAC GGTGCCAAAA CAGAAATCAC TTGGTGGGCA	420
TTCCCAGTAT TTACCCAAGA AAAAAGTGGT GACGGTGTG GAACTTATGA AAAATCAATC	480
ATCCAAGCGT TTTGAAAAAG CAACCCAGAT ATAAAAGTGA AATTGGAAAC CATCCACTTC	540
CAGTCCAGTC CTGAAAAATC ACAACAGCCA TCCGAAGCAG GAACAG	586

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TGGTAGTTCT TCCTAGTGCA GGGGCTGTAG ACCCAGTTGC GACCCTAGCG CTGGACTAGT	60
CGAGAGGGTG TTGTTGAAAA TGGATGGNTA TCGCTATGTT GGTATCTAT CAGGTGACAT	120
CCTCAAAACG CTTGGCTTGG ACACTGTTTT AGAAGAAACC TCAGCAAAAC CTGGAGAGGT	180
GACTGTAGTC GAAGTTGAGA CTCCTCAATC AACAACAAAT CAGGAGCAAG CTAGGACAGA	240
AAACCAAGTA GTAGAGACAG AGGAAGCTCC AAAAGAAGAA GCACCTAAAA CAGAAGAAAG	300
TCCAAAGGAA GAACCAAAAT CGGAGGTAAA ACCTACTGAC GACACCCTTC CTAAAGTAGA	360
AGAGGGGAAA GAAGATTCAG CAGAACCATC TCCAGTTGAA GAAGTAGGTG GAGAAGTTGA	420
GTCAAAACCA GAGGAAAAAG TAGCAGTTAA GCCAGAAAGT CAACCATCAG ACAAACCAGC	480
TGAGGAATCA AAAGTTGAAC CACCAGTAGA ACAAGCAAAA GTCCCAGAAC AACCCTGTGA	540
ACCTACACAA GCTGAGCAAC CAAGTACACC AAAAGAATCA TCACAACAAG AAAATCCTAA	600
AGAAGATAGG GGAGCGGAAG AGACACCGAA ACAAGAAGAT GAACAGCCAG CAGAAGCCCC	660
AAGAAATCAA GGTGAAGAA CCAGTAGAAT CAAAAGAGGA GACTGTTAAT CAACCTGTTG	720

AACAACCAAA	AGTGGAACG	CCTGCTGTAG	AAAAACAAAC	GGAACCAACA	GAGGAACCAA	780
AAGTTGAAGT	AACAAGTATT	CCCCAACTA	CTCGCTATGA	GGAAGACCTT	ACTAAGGAAC	840
ACGGAACGCG	TGAAGTTGTT	AAGGAAGGTA	AGAATGGCAG	TAGAACAGTT	ACTACTCCAT	900
ATATCTTGAA	TGCGACAGAT	GGTACGACTA	CAGAAGGCAC	TTCGACAACT	GATGAAGCTG	960
AGATGGAGAA	AGAGGTTGTT	CGTGTGGCA	CGAAACCCAA	AGAAAAATTA	GCTCCAGTCT	1020
TAAGTTTGAC	AAGTGTTACA	GATAATGCAA	TGTTGCGTAG	TGCGAGACTT	ACTTATCATT	1080
TGGAAAATAC	AGATAGTGTT	GATGTGAAAA	AAATTCATGC	TGAAATTAAA	AATGGCGATA	1140
AGGTTGTCAA	AAC TATTGAC	TTATCTAAAG	AGAGATTATC	AGATGCTGTT	GACGGTCTTG	1200
AACTTTATAA	AGATTATAAG	ATTGTGACGA	GTATGACCTA	TGATAGAGGT	AATGGTGAAG	1260
AAACCTCTAC	GTTGGAAGAA	ACTCCACTAC	GATTAGACCT	CAAGAAGGTT	GAATTGAAAA	1320
ACATCGGCTC	TACTAATCTC	GTCAAAGTAA	ATGAGGATGG	TACTGAGGTG	GCAAGTGACT	1380
TCTTAACAAG	TAAACCTGTG	GATGTGCAGA	ATTACTACCT	CAAAGTAACT	TCCCGTGATA	1440
ATAAAGTTGT	TTCCCTCCC	AGTTGAAAAA	ATTGAAGAGG	TGACTGAGGA	AGGTCCACCA	1500
CTTTACAAAG	TCCCTGCTAA	GGCCCTAATT	TGAT			1534

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CGGATTTGTT	TATCTCAAGA	AGAGTCGCGA	TATTCTCCGT	GAAAGTTCAG	AATTGATTAN	60
CCAAACGGTA	GAAGATTATC	TTCAAGGAGA	TGACTTTGAC	TGGGCAGATC	TTAAAGGGAA	120
GGTTCGANAT	AATTTGACCA	AGTATCTCTT	TGACCAAACC	AAGCGTCGTC	CANCTATTTT	180
ACCAGTAGTC	ATGGAAGCAA	AATAATCGTT	GAAATAAACA	GAGAGAAAGT	CGAGTTTCGG	240
CTTTTTCTTA	TAGAAAAATA	GAAGGAGAAA	ATCATGGCAG	TAATGAAAAT	CGAGTATTAC	300
TCACAAGTAT	TGGATATGGA	GTGGGGGGTG	AATGTCCTCT	ACCCTGATGC	CAATCGAGTG	360
GAAGAACCAG	AGTGTGAAGA	TATTCCCGTC	TTGTACCTTT	TGCACGGGAT	GTCTGGAAAT	420
CATAATAGTT	GGCTTAAGCG	GACCAATGTA	GAACGCTTGC	TTGAGGAAC	TAATCTCATC	480
GTTGTTATGC	CCAATACCAG	CAATGGTTGG	TACACCGACA	CCCAGTATGG	TTTTGACTAC	540
TACACGGCTC	TAGCAGAGGA	ATTGCCACAG	GTTCTTGA	CGCTTCTTCC	CTAATATGAC	600
TAGCAAGCGT	GAAAAGACCT	TTATCGCTGG	TCTTTCTATG	GGAGGCTACG	GCTGCTTCAA	660
ACTGGCTCTT	ACGACAAATC	GTTTTTCTCA	TGCAG			695

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1096 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CTCATCCAAG	AATAGCATAA	AAGAACTCTT	CTGTTTTTTC	TTGAGGAACG	AGAAAGTCAG	60
CAATCTCCAT	TCCACGATCC	ATCAAATCCT	CTAAAGACAT	CGTGATTTTT	AAAGTAGTAT	120
CACTAATTTG	TTTCATTTTC	ATTGCTAGTA	ACCTCATACT	TTCAGTTCTA	TCTATTATAC	180
TAGATTTTTA	CGATTTTATC	AAAAGAAGGC	TCCTCTATAC	GGATAGATTT	TCCCTAGGGT	240
CTTTCTATAG	GAGACTCCAA	GAGAAAATTT	CTGCAGACAG	ATAGAAAAAG	CCTTCAAAAT	300
CGGCTCTTAG	CCGATTTTGA	AGACCTTATA	CATCAGAATA	CTTATAATTT	AAAGGTTGCT	360
ACACCGAGGA	TAGAACGATT	TAAGTTTCTG	AGAATTTGAA	GACTTTGCTC	AAATTTCTTA	420
TAACGAATTC	ACTCCGTACT	CTTCAACAAG	AAGGACTGTA	TCTCTTTCCA	AAAGAGATGA	480
TACATCCTGC	AAATCTACAA	ATGCATTCCCT	TTTAAAGCTT	CTTGACTCTG	TTTCAATTTA	540
TCTAGGATAG	CTTTATTTGA	GCTAACGATG	GTCAATTCCT	GTCCAGTATT	TTTGTATGAC	600
AAAACATCTG	CTAGGTTAGC	AATTGTTGTA	ATCTCTGTTA	CAAAATCAAT	TTGATACTGA	660
GAAAAATCAC	CTACTCTATT	GATTGTTGGA	TTAAAGAGAT	AAACTAACAC	ATTTCCCATC	720
ACAACCAAAA	TCACACAAAC	CACTCCAATA	ACAACATAAC	GAAGAATCAG	ATTTTTCACA	780
TTTAAGCCAA	GCGCTGTTTC	ACCATTTGCG	TTCAATTCTT	TAGAGTTGAT	GGTTTCCAGT	840
TTTTCAATTT	TCACATTTGC	ATAAGCATGT	TTAAATTTCT	CAATCAACCC	ATCAATTTTT	900
TTCTCTAACA	AGTCATTGGC	ATCTTTACTT	GATGTCAAAA	TTTTCACACC	AACCCCTGCA	960
TCGTCAATCA	TATAGTAGAC	GGTCAATTTT	TTCCACCAAT	AGTCATTTCG	TGAATTTTTC	1020
AAGGTTGTTT	CCGTCGTGTC	TAATTCACTG	GCAATTTTTT	TCAACTCACT	GGGTTCTACA	1080
TCATTGAAAA	GATAAG					1096

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1037 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TCCCCATCCC	AGTGGGCAGC	AGCATTAGTC	TGTACTTCTG	CGTCGTTGCG	TTTTATTAGA	60
AGACTGATTT	TGCTTTGAAC	TACTTGAAGC	TGTCGTTGTA	TCCTGCGAAG	TTTTTGCTAA	120
CTTCAGTTTC	ATTTGCAGCG	ACATGACTAG	TTGCCAAGCC	TAGTAAACAG	ATACTTGCTA	180
ATCCAATTTT	TGTTTTCAAT	CTTTCCTCTC	CTATAAAAAA	TGTAACAGAC	ATCTGAATGC	240

TGTTCCACCT	AGCTTTTGCT	ACTTACTGAT	TATTTTACAA	AGTCAAGCAA	AGCCAAGAAG	300
CTTTCAGCTT	CAAGTGACGC	ACCACCTACA	AGGGCACCCT	CAACGTCTGG	GCAAGCCATG	360
TATGAAGCAA	CATTTTCAGG	TTTAACAGAA	CCACCGTATT	GAACACGAAC	TTTGTCTGCG	420
ACTTCTTGAC	CAAAGTCAGC	AGCTACAACG	TCACGAACAA	CTTTACACAT	TTTTTGTGCA	480
TCGTCTTGTTG	AAGCTGATTT	ACCAGTACCG	ATAGCCCAGA	TTGGCTCATA	AGCGATAACT	540
GAGGCAGCAA	CTTGTTTCAGC	AGTCAATCCA	GCCAATGCAG	CAGATACTTG	AGCACCTACG	600
AATTCAGCAG	CTTTACCAGC	TTCGTAAGTT	TCAAGTGATT	CACCACAACA	GATGATTGGA	660
AGCATACCGT	TCGCAAAGAT	TGCTTTTGCT	TTTTTGTTGA	TATCTTCGTC	AGTTTTCATGG	720
AAGTAGTCAC	GGCGTTTCTG	AGTGACCGAT	AACAACGTAG	TCAGTACCGA	TTTCTTTCAA	780
AACTTGTGGG	CTAGTTTCAC	CAGTGAAAGC	ACCTGCATTT	TCTCCGTAGC	AGTTTTGAGC	840
AGCGACTTTT	AAGTTTGAGC	CTTNGGCAAC	AGCAAGNACA	GTTGTCAAAT	CAAGAGCTGG	900
AGCAGNGATA	CCTGCTTCAA	CAAGATCTGA	TGAAGGAAGT	TTTGATGCAA	CTGCTTCAAC	960
GAATGNTCCA	GCTTNTTGGG	GATTTTGTG	CATTTTCCAG	TTACCAGCGA	TAAATGGTTT	1020
ACGTGACATT	TCACATA					1037

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CTTATCGTAC	TAAGGATGGC	AGTGTTCAAC	TGTTCCGTCC	TGATGAAAAT	GCTAAACGCC	60
TGCAACGTAC	ATGTGACCGT	CTCTTGATGC	CAACAAGTTC	CGAACAGACA	TGTTTGTAGA	120
AGCTTGTAAG	GCAGTTGTCC	GTGCGAATGA	AGAATACGTA	CCACCATACG	GAATAGGTGG	180
AACTTTATAT	CTTCGCCCTC	TTTGTATTGG	TGTCGGAGAT	ATTATCGGGG	TAAACCGGC	240
AGAAGAGTAC	ATTTTCACCA	TCTTTGCTAT	GCCAGTTGGA	AATTACTTTA	AAGGTGGTTT	300
GGTCCCAACC	AACTTCTTGA	TTCAGGATGA	GTACGACCGT	GCAGCACCAA	ATGGTACAGG	360
TGCGGCTAAG	GTTGGTGGAA	ACTATGCTGC	AAGTCTCTTA	CCAGGAAAAA	TGGCCAAGTC	420
ACGCCATTTT	TCAGATGTTA	TCTATCTGGA	CCCATCAACT	CATACAAAGA	TTGAAGAAGT	480
CGGATCAGCT	AATTTCTTTG	GAATTACAGC	TGATAATGAA	TTTGTAAACAC	CATTGAGTCC	540
ATCTATCTTG	CCATCTATTA	CCAAGTATTC	CTTGCTTTAT	TTGGCAGAAC	ATCGCTTGCG	600
ATTAACCTCT	ATTGAGGGTG	ATGTTCCAAT	TGATAATCTT	GACCGTTTTG	TAAAGGCAGG	660
TGCCTGTGGT	ACAGCAGCGG	TTATTTCTCC	AATTGGAGGT	ATTCAACATG	GTGATGATTT	720
CCATGTTATT	CTATAGTGAA	ACAGAAGTAG	GTCCTGTGAC	ACGTAAATTA	TATAATGAAT	780
TGACGGGTAT	TCAGTTTGGC	GATATTGAAG	CGCCAGAAGG	TTGGATTGTA	AAAGTAGATT	840
AAAATAAACC	AAAGGAGATT	TTTTATGAAA	TAGAAAAAGT	GGCTCTTAAC	AGCAGGAGTG	900
GTCCTGAGCA	CGTCAGCTAT	TTTAGTGGCT	TGTGGAAAAA	CTGATAAAGA	AGCAGATGCA	960
CCGACAACAT	TTTCTTATGT	CTATGCAGTA	GATCCAGCAT	CATTGGGCTA	CAGTATAGCG	1020

ACTCGAACAT	CGAGGACAGA	CGTTATTGGA	AATGTTATTG	ATGGTTTGAT	GGAAAATGAT	1080
AAATACGGCA	ATGTTGCTCC	TTCTCAAAAA	GACTATGATT	TGAACAGTAC	AGGATGGGCT	1140
CCAAGCTATC	AAGATCCAGC	GTCTTACTTG	AATATTATGG	ATCCAAAATC	TGGTTC TGCC	1200
ATGAAACACC	TTGGCATTAC	GAAAGGAAAA	GATAAGGATG	TTTGTAAC TA	AACCTGGTTT	1260
GGATAAATAT	AAGAAATTGT	TAGAAGATGC	TGTTTCTGAG	ACCACTGACC	TAGAGAAGAG	1320
ATATGAAAAA	TATGCCAAAG					1340

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CTCTGACGGC	GTGCCACTT	AAGAAGAGTA	TCAAAAAGAA	AAATAGAAAA	TTAACTAACA	60
AGGNAGAAAA	ACACATGTCT	AAAATTATCG	GTATTGACTT	AGGTACAACA	AACTCAGCAG	120
TTGCAGTTCT	TGAAGGAACT	GAAAGCAAAA	TCATCGCAAA	CCCAGAAGGA	AACCGCACAA	180
CTCCATCTGT	AGTCTCATTC	AAAAACGGAG	AAATTATCGT	TGGTGATGCT	GCAAAACGTC	240
AAGCAGTCAC	AAACCCAGAT	ACAGTTATCT	CTATCAAATC	TAAGATGGGA	ACTTCTGAAA	300
AAGTTTCTGC	AAATGGAAAA	GAATACACTC	CACAAGAAAT	CTCAGCTATG	ATCCTTCAAT	360
ACTTGAAAGG	CTACGCTGAA	GACTACCTTG	GTGAGAAAGT	AACCAAAGCT	GTTATCACAG	420
TTCCGGCTTA	CTTCAACGAC	GCTCAACGTC	AAGCAACAAA	AGACGCTGGT	AAAATTGCTG	480
GTCTTGAAGT	ANGACGTATT	GTTAACGAAC	CAACTGCAGC	AGCTCTTGCT	TATGGTTTGG	540
ACAAGACTGA	CAAAGAAGAA	AAAATCTTGG	TATTTGACCT	TGGTGGTGGT	ACATTCGACG	600
TCTCTATCCT	TGAATTGGGT	GACGGTGTCT	TCGACGTATT	GTCAACTGCA	GGGGACAACA	660
AACTTGGTGG	TGACGACTTT	GACCAAAAAA	TCATTGACCA	CTTGGTAGCA	GAATTCAAGA	720
AAGAAAACGG	TATTCGACTT	GTCTACTGAC	AAGATGGCAA	TGCAACCTTT	GAAAGATGCG	780
GCTGAAAAAG	CCAAGAAAGA	CCTTTCTGGT	GTAACCTCAA	CACAAATCAG		830

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GTGGTGGTTT	GACTGCCCTT	ATCGAAGCAG	GTTTCGAANT	CTAAGACANA	AGCAGGTTAC	60
GCTCCAGAAT	TGGCTTAACT	TTGAAGTTCT	TCACGGAAAT	GAAATTGATC	GTTGACTTGA	120
TCTACGAAGG	TGGATTCAAG	AAAATGCGTC	AATCTATTTT	AAACACTGCT	GAATACGGTG	180
ACTATGTATC	AGGTCCACGT	GTAATCACTG	AACAAGTTAA	AGAAAATATG	AAGGCTGTCT	240
TGGCAGACAT	CCAAAATGGT	AAATTTGCAA	ATGACTTTGT	AAATGACTAT	AAAGCTGGAC	300
GTCCAAAATT	GACTGCTTAC	CGTGAACAAG	CAGCTAACCT	TGAAATTGAA	AAAGTTGGTG	360
CAGAATTGCG	TAAAGCAATG	CCATTTCGTTG	GTAAAAACGA	CGATGATGCA	TTCAAAATCT	420
ATAACTAATT	AGAAATATAT	AGCGCTGGAG	ATGATTTTAT	GAAAAAGATT	ATGAGAAAAA	480
TTGCATCGTT	ATTATTGGTT	CTAGTTGTAT	AATGTAATTA	CACCGTCGGT	AATAGTGCTA	540
GCAGACCAAA	ATAAAGCAGA	TTGGTCGTAT	GATGAAAATA	CTGTAATTAA	CATTTATGAT	600
GATGCTAATT	TTGAAGATGG	TAGGTTGCAT	ATGACCTTTG	AACAATTCTT	CAAATTGGCA	660
CAAATAG						667

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CGGTTCCAGA	NACTGGTATG	GCTAGGAGTC	GCGACAAAGT	GTATCTTATG	ATGGTCGATT	60
TGATACTCAA	TACGCTCAAT	ACTTACGGAA	AGAATAAACG	ATCATTGTCA	ACCGGAATAG	120
TATGATAATC	GTTTCTTGGT	GGAATAAGTT	CAATCTTATC	CTTCTTAGGC	ACAATAATGG	180
AAGAGCCCAG	TGTTTCGATA	ACACGATTAT	TAAGGCTGGC	AATTTCCGTT	AATTGCAAAG	240
CTTCAATGGT	AGGGTGTAAG	ACAGCACCAC	CAAGAGACTA	GTTATAGGCA	GTACTACCAG	300
TCGGTGTCTG	AACTGTTAGC	CCGTCTCCAC	GAAAACGTTT	AAAGGGAACA	CCATTTATTA	360
CAATATCTGC	CACCATGGTT	CGATCAGACC	TGCGGATGCT	GGCTTCGTTG	AGTGCTCTGA	420
AAATCTTAAC	TTCACCATTT	TCAAGAAAGA	CCTTCACATT	CAGAACAGGG	TAAGAAACCC	480
TTGCCCCAGT	ATCTAGCTGC	AAATTAGTCA	CTAGCTTGTC	CAACTCAAAA	TCACGATAAT	540
CTGTATAGAA	GCCCCAATGT	CCAGTATGAA	GACCGATAAA	GCGGACCTTG	TCAAGCTGAT	600
TTTCGTAATT	ATGAAAGGCC	GACAAGAGCA	TACCATCCCC	GCCAATGGAA	ATGACAATAT	660
CCGGATTGGT	ATCATTGAGT	TATAAACTGA	TTTCTCTTCA	AACGATCTCG	CAATTCATAC	720
AAAACCCTTT	GACTCTGCGG	TTTTCTATTG	GCTATCAGAT	CAATTCGTTT	ACCTGTATTC	780
TTCATCTGTA	TCGTCACGTN	NTCCAACACC	GTCATTTAAT	TTTCTACTCA	AAGGATCAAA	840
AAGTGCCTGG	GCTTCTTGGA	TATCATCAGC	AATTTACCCC	ATTTCTTCAT	CCAAGTATG	900
GGCGATTCTA	GCTGTAATTT	CCAGTCGCTT	CTTAATCTCA	TCTGGGAAAT	CCCCTTGGTA	960
CTTGTAAGTT	AGAGAAATGTT	CTATCGTTGC	CCAGAAATTC	ATGGCCAAAAG	TACGAATTTG	1020

AATTTCTGCC	AAAATAGTCT	TAGCTCCATT	GATGGTATCA	ACCGTATATT	CTACTACCAC	1080
ATGATAGGAA	CGATAGCCTG	ATGCTTTTCT	ATGAGTAATG	TAATCTCGCT	CCTGTATGAT	1140
TCGCATATCC	TGACGCTTGT	GCAAAATATC	CACTACTTCC	TTGACGTCAT	CTACAAACTG	1200
AACCATCACA	CGTAAGCCAG	CAATATCCTG	CAAATCGTGT	TCCAAGGTCG	CATAAGTAAT	1260
GCCACGACGA	GCCATTTTTT	CTTTGATGCT	CTCAATTGGC	TTGACTCGAC	CGGTCACAAA	1320
CTCAATTGGA	GAATGCTTAT	TTTGCTTACG	ATATTGCTTA	CGAATACCAC	GAAGTTTAAT	1380
CTTTAACTCA	CCAACAG					1397

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CTCCCATGAC	ACCTGCACGC	TCCGTACGGG	CCACGTGCTT	TTTAATCCGT	TCAACAACTT	60
CATAACCCGC	TTCAACATCC	ACACCCGACT	GGGCATATGC	ATTTTTATTT	GTCATTTGTT	120
TTTTCTTTT	CTTTAATGGA	GAATCTGTCG	CCTACTTGTA	AAAAC TG GTC	TTTTCTTCCA	180
AACTTCTACG	ATAGTCTTCT	TCGTAGTCAT	AGAGAGGCGT	TGGGTAGTCA	CCGTCAAAGT	240
AAGCGACACA	GAGACCACCG	TTCGGCGCAT	CTGTTTCGAT	ACCAATCGAC	TCAATCAAGC	300
TATCAATTGA	AAGATAAGTC	AGACTGTCCG	CACCAATGAT	TTGGCGAGTT	TCTTCGACCG	360
TATGATTGGC	TGCAATCAGC	TCCTGACGGG	TCTGGATATC	AATCCCGTAG	AAACATGGAT	420
ACGCTAGTGC	AGGACTTCCA	ATGGCAACGT	GAACCTCAGT	CGCACCCGCT	TCTTTCAAGA	480
GCTGAACGAT	ACGACGAGAG	GTTGTTCCAC	GTACAATGGA	ATCATCCACC	ATGACCACAC	540
GTTTGCCTTT	GACAACACCC	GAAACAGCAG	ACAGTTTCAT	CCGCACTCCT	TGCTCCCGCA	600
ATTCTTGAGT	CGGTTGGATA	AAAGTTCGCT	GGGTGTATTG	GTTTTTGATC	AGACCCATTT	660
CATTTGGTAA	GCCTGATTCT	TCCGCAAATC	CCATAGCCGC	GCTTAGGGAA	GAATTGGGCA	720
CACCAACTAC	AATATCTGCC	TCATGCTTAA	ATTCTCGCGC	CAATTGCGCT	CCCATTCTCT	780
TACGTGCCGT	ATGGACATTG	ACCCGTGGAT	ATTAGAATCA	GGGC		824

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1020 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTTCTTCCTT	GGTACTTCCT	CAATTGGATT	ACCTTTGGCA	TGCTAGTTT	TTCACTCCTA	60
CCTTATATCC	AAGGCACTAA	AATTATGTTT	TACCGAGCAG	TATTGGCTCG	AAAACGTCCA	120
AAAGCTTGAA	GGTTTTCCCC	TCAAGCTTTT	TTCTATCAAT	GAATTTCTCC	GCCTACCAAC	180
GTGAGTTCCT	GATCTCCATG	TTCTATCATA	GCGCCGATTG	CTGCTTCTAT	CCCTCGCCGA	240
ATATCCACTA	AACTCATAGT	TGGAGTAGTC	GGTCTGTTCA	CCACCTGTTC	CATCATATAA	300
GGAATATGCA	TAAAACCTGC	CTTAACATAT	GGGAATTTCT	TTTCTACCAA	ATAGAGAGCC	360
TGATACATCA	AATGACTGCA	AACAAAAGTC	CCTGCACGTA	TTGGAAACAG	ACTGCCGGTA	420
AGTCCTTCTT	TTTTATTAGC	TTGTACCATC	GCTTTGATAG	GTAAACTACT	AAAATAGGCC	480
GATGCTCCAT	CAATACGAAT	CGGTGTATCA	ATTGGTTGAT	TGCCTTCGTT	ATCAGGTATG	540
CGAGCATCAT	CTTGATTAAT	AGCCACTCGT	TCAGGTGTTA	AGCCGGTCCT	GCCGCCTGCT	600
TGTCCAATAC	AAAGTACAGC	ATCTGGTTGA	TATCGTAATA	TTTCTGCCTC	TAAAACCTTCT	660
GACGACTTAT	AAAAAACCGT	TGGAATTTCT	ACCCAGCGAA	CTTCAGCCCC	ATTAATCTCA	720
GATGGTAATA	ATTTTACAGC	CTCCAAAGCT	GGATTAATCT	TTTCACCTCC	AAAAGGATTA	780
AAACCTGTAA	CCAATATTTT	CATTTTATTT	TCCTTTACTA	AAATGCGAGA	AAGTACATTA	840
AGAATATGTG	AATAACAATC	ATTACTAGAG	CAACACCTGC	TTGAGCCTTT	ATAACGCCAT	900
TCTGATCTTT	CATATCCATC	AATGCTGCTG	GTAGAGCGTT	AAAATTAGCA	GCCATTGGGG	960
TCAATAAGGT	CCCACAATAA	CCTGCTGTCA	TGGCAAGAGC	ACCAGCCACA	ATTGGATTAG	1020

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTCGTAAAAA	CACTAAAGGA	GGTAAATAAC	CAATGTTAGT	ACCTAAACGT	GTAAACACC	60
GTCGTGAATT	CCGTGGAAAA	ATGCGCGGTG	AAGCAAAAGG	TGGAAAAGAA	GTAGCATTCG	120
GTGAATACGG	TCTTCAAGCT	ACAAC TAGCC	ACTGGATCAC	TAACCGCCAA	ATCGAAGCTG	180
CTCGTATCGC	CATGACTCGT	TACATGAAAC	GTGGTGGTAA	AGTTTGGATT	AAAATCTTCC	240
CACACAAATC	ATACACTGCT	AAAGCTATCG	GTGTGCGTAT	GGGATCTGGT	AAAGGGGCAC	300
CTGAAGGTTG	GGTAGCACCA	GTAAACCTG	GTAAAGTGAT	GTTGCGAAATC	GCTGGTGTAT	360
CTGAAGAGAT	TGCACGTGAA	GCGCTTCGAC	TTGCTAGCCA	CAAATTGCCA	GTTTAAATGT	420
AAATTCGTAA	AACGTGAAGC	AGAATAAGGA	GAAGGCATGA	AACTTAATGA	AGTAAAAGAA	480
TTTGTTAAAG	AACTTCGTGG	TCTTTCTCAA	GAAGAACTCG	CGAAGCGCGA	AAACGAATTG	540
AAAAAAGAAT	TGTTTGAAC	TCGTTTCCAA	CCTGCTACTG	GTCCAATTGG	AAACAAACAG	600

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

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CTTCAGCGAC ATATCTATCC ACAACTTCTC TCGATTCATG TTCCTCTGAA AATGCCTGAA      60
ATTTTAATTG ACTAATTTGA TCCTGATACG AACTATCTGC TAACAAAAC TCAAGATGGG      120
AAACATTTGC TAACGGATAA GGTCTTCTAT CCTTACCTAA CCAAGTTTCT GTCTCTTCAT      180
CCTCTATTAG TCCCCAGTTA CTGGCAAAGT CAGGATGATT CTCTAAAAAA ATACGTTCTG      240
TCTGAAAAGT GACTGACCGA ATGGGGAAAG AAGCTGTTCC TCTCTCAAAA CTAGTAAACA      300
ATGCACGCGC AATCCCCTGA CGGCGATGAC CTGGATGAAC CAGTATCGTC ACTTCTACAT      360
CTTGGTCATC TGCATAGACA GTTAATAAAC CAACAAGTTC GCCTTTTTC TAATAAAGGA      420
AAAAGGCGGG CATGTTTGGA TCAAAATTAA GCATGTTAGA GAGATAGGGA TCGCGATAGG      480
TACCGTCATA GTTTTGCAA CAGTTAATTA CTTTTTTCGC CTCAGATAGC TCTTCTTGGC      540
TTAACTTGTT TCTTGCTTGA ATCATATAGG TATCCTCTAC AAACCAGACG ATCTGTGACT      600
GGCATCTTTA GCCTGCTCGA GTTTATTGAC ATAATACTCC CGTTTTTCTT CGACTTCGTG      660
AATAACAGGC TCATCTTTCT TACCATGAAG ACGGACAATC TTGGCCGGAA TACCGACAAC      720
CGTCACATCA CTAGGTACAT CTGCTACGAC AACTGCTGCA GCACCGACCT TGGCATT TTC      780
ACCAATTTCC ACAGGCCCGA TAAC TTGGGC ATGGGCTGAT ATGAGGGCTC CTTTTCGTAC      840
AGTCGGATGG CGTTTGCCAC AGTCTTTCCC TGTTCCTCCG AGAGTCACTC CGTGATAGAG      900
AAGAACGCCT TTTTCAACAA TCGCTGTCTC TCCAATCACC AGACCAGAAC CATGGTCAAT      960
AAAGACACCT GAATCAATCT GGGCTCCTGG ATGAATCTCA ATCTGAGTCC AAAAGCGCCA     1020
AAACTGACTG TGCATACGAG CTAAGAGTTT GAAGTCGTAC TTCCAGAGAA AATGCGAGAG     1080
ACGGTGGGCC GCCAAGGCCT TGACACCTGG ATAAGTCAGC AAAACCTCCA AAGTGGTGCG     1140
GGCCGCTGGA TCATTTTCTT TTACGATATC AATGGTTTCG CGCCACCACC CCATACATTT     1200
CTCCTTTTCT TACTCTGAAT CTT

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(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGTGAGTGCC	TTTATTAGCG	GAGCTTCTCA	AGTGATTGTT	GCCTTGATTA	TCTTCCTTTC	60
ATGCTCTTTT	ATCTCTTGCG	TGATGGGAAA	GGCTTGCGTA	ACTATTTGAC	CCAATTCATT	120
CCAAGCAAAT	TGAAGGAACC	TGTTGGACAA	GTTCTATCAG	ATGTGAATCA	ACAGTTGTCC	180
AACTATGTTT	GAGGGCAAGT	GACAGTGGCT	ATTATTGTAG	CAGTAATGTT	TATCATCTTC	240
TTCAAGATTA	TTGGTCTACG	CTATGCGGTT	ACGCTGGGGG	TTACTGCTGG	TATTTTAAAT	300
CTGGTCCCTT	ATCTTGGTAG	CTTTCTAGCC	ATGCTTCCTG	CCCTAGTATT	GGGTTTGATT	360
GCTGGTCCAG	TCATGCTTTT	GAAAGTAGTG	ATTGTCTTTA	TTGTAGAACA	AACTATTGAA	420
GGCCGTTTTG	TCTCTCCATT	GATTTTGGA	AGTCAATTAA	ACATCCACCC	TATTAATGTT	480
CTCTTTGTTT	TGTTAACTTC	AGGATCTATG	TTTGGTATCT	GGGGAGTTTT	ACTTGGTATT	540
CCGGTTTATG	CCTCTGCTAA	GGTTGTCATT	TCAGCCATTT	TCGAATGGTA	TAAGGTAGTC	600
AGTGGTCTAT	ATGAATTAGA	GGGTGAGGAA	GTCAAGAGTG	AACAATAGTC	AACAGATGTT	660
ACAGGCTTTG	GAGGAGCAAG	ATTTAACTAA	GGCTGAGCAT	TATTTGCGCA	AAGCTTTAGA	720
AAATGATTCA	AGTGATCTTC	TGTATGAGTT	GGCAACTTAT	CTTGAAGGGA	TTGGTTTCTA	780
TCCTCAGGCC	AAGGAAATTT	ACCTGAAAAT	TGTAGAAGAT	TTCCAGAGG	TTCATCTTAA	840
TCTAG						845

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CTATGGATTA	ATCTTCTTCT	ATCTTATCCT	GTCCTAAAT	ATGTTGGTAG	AAAAATGAAG	60
CAGTTGTTAC	GAGTGTCTGT	ATTGGAAAAA	AATTTTGTCT	ATACAATTCT	TTAAATGATA	120
TGAAGACTAG	GAATGCCAAA	ACACTGACAT	ATTTCGTTTA	AAGCCTATCC	AGTCTCTTCA	180
ATTGTATTTG	TAGAAATGCT	ATCAGTAATA	TATTCGCGAA	CACTATGATT	TACAACAGTG	240
TGGTCGTACA	TCTTTGTAAC	TTTATTATAC	AACAACCATT	TACAGGTGTA	AAGTTGAGCA	300
GTGTCTTTAG	TAAATTTAGG	GACTTGTTTT	GTCATAGTTT	TGATACCTGT	ATTCGTTGTT	360
TCATGAGTAT	TTGACGTTTC	TTTTCATGTA	GGCATTTCOA	CAATTAGAAT	GATATTTTTC	420
CGAGGATGAA	CTTATATATT	ATGACTTTTT	AGAGTTATGA	TGCCTCTTGA	TTTGACTATC	480
GCTATCAATT	TCATCCACTT	TTACAGTTTC	ATGCAACATA	GCGAGAAGGC	GGTTTCCTAT	540
ATGGAAGTCG	TCTTGTTTTT	ATATTGTCTA	AATACGAGAT	ATTTACTACA	GGTTGTAGAT	600
ATTGCAAGCT	CAAAATGATAT	TATTTTAGAG	GAGGAGACAA	GTGAAATAAT	GCCTGGTGAG	660
TTAGATGAAA	TAAAAAGTAA	GGAGTTGAAA	GTAAGTTTTC	NTTGTGCAGG	GTCTGGAACA	720
AGTGCGCAAT	TAGCCAATGC	AATTAACGAG	GGCGCTCNAT	TAGCAGAAGT	TAGAGTGATT	780
GCGAATTCAG	GAGCGCACGG	AG				802

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

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CTGGGACTCT CTTCTAGAA GTCATGCAAG AATATTTTGA TCAAAAGAGG AAATCATGAA      60
AAAAAGAGCA ATAGTGGCAG TCATTGTACT GCTTTTAATT GGGCTGGATC AGTTGGTCAA      120
ATCCTATATC GTCCAGCAGA TTCCACTGGG TGAAGTGC GC TCCTGGATTC CCAATTTTCGT      180
TAGCTTGACC TACCTGCAA ATCGAGGTGC AGCCTTTTCT ATCTTACAAG ATCAGCAGCT      240
GTTATTCGCT GTCATTACTC TGGTTGTCGT GATAGGTGCC ATTTGGTATT TACATAAACA      300
CATGGAGGAC TCATTCTGGA TGGTCTTGGG TTTGACTCTA ATAATCGCGG GTGGTCTTGG      360
AAACTTTATT GACAGGGTCA GTCAGGGCTT TGTGTGGAT ATGTTCCATC TTGACTTTAT      420
CAACTTTGCA ATTTTCAATG TGGCAGATAA CTATCTGACG GTTGGAGTGA TTATTTTATT      480
GATTGCAATG CTAAGAGAGG AAATAAATGG AAATTAAAAT TGAAACTGGT GGTCTGCGTT      540
TGGATAAGGC TTTGTCAGAT TTGTCAGAAT TATCACGTAG TCTCGCGAAT GAACAAATTA      600
AATCAGGCCA GGTCTTGGTC AATGGTCAAG TCAAGAAAGC TAAATACACA GTCCAAGAGG      660
GTGATGTCGT CACTTACCAT GTGCCANAAC CAGAGGTATT AGAGTATGTG GCTGAGGATC      720
TTCCGCTAGA AATAGTCTAC CAAGATGAAG ATGTGGCTGT CCTTAACAAA CCTCAGGGAA      780
TGGTTGTGCA CCCGAGTGCT GGTACATACCA GTGGAACCCT AAGTAAATGC CCCCATGTA      840
TCATATTAAG GACTTGTCGG GTATCAATGG GGTCTGCCT CCANGGATTG TTCACCCGTA      900
TTGATAAGGA TACGTCACGT CTTCTCAT

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(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

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CTCTTTTACA GAGGTGTTTC CTATTTTGTG CTTCATTTT TGGGGCAAGG AATTGTAGAT      60
GGGGATGGCA ATCCTATCTT TTTATTGATT ATGATATTCG TTTGCTTCAT AGTTTATAGTC      120

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TTTTTGAAAT	GGTTAGACTA	TGATTTCACT	AGATTGAGAA	GGGAGTTTCT	AGATACAGGT	180
TTTCAAAAGT	CTCTTACTAA	GATTAAGTGG	GCAATGGGGG	CTTATTATCT	AGTGATGCAA	240
AGTCTATCTT	ACCTTGAATA	TGAACAAGGT	ATTCAATCAA	CGACTGTTTCG	CCATCTCATC	300
CTAGTGTTTT	ACCTACTCTT	TTTTATGGGG	GGTATCAAGA	AATTGGATAC	CTATTTGAAG	360
GAAAAACTTC	AGGAGGAACT	GAACCAAGAG	CAGACCTTGC	GCTACAGAGA	TATGGAACGC	420
TATAGTCGGC	ATATAGAGGA	ACTTTACAAG	GAAATTCGGA	GTTTTCGCCA	TGACTACACT	480
AACCTCTTAA	CCACTTACGT	TTGGGCATTG	AAGAGAAGGA	TATGGAGCAG	ATAAAAGAGA	540
TGTACGACTC	GGTCTTAAGG	GATTCCAGTC	AGAAATTGCA	GGACAATAAA	TATGACCTGG	600
GCAGATTGGT	GAATATTNGT	GACCGTGCCC	TCAAGAGTCT	CCTAGCTGGA	AAATTTATAA	660
AAG						663

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 653 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTAGATTAAT	CTGATATTTT	TTTTTGGCAA	ACCAAATGCT	TCCTATCAGA	AAAGCTAGCA	60
ACAGCAACAT	GGTAATAATG	ATATGAATGG	TCATTTTCTT	CTCCTATTCT	GCCTTTTCAA	120
TATCTTTTTT	CATCTCGTCA	ACATTGAACT	TAGCAAACAA	GTATTGACGG	TCTTGGACTG	180
GGAAACGTTG	GTCCAACCTG	TCAACTGCTC	CCACCTCGAT	AATGCCTTCC	TTGATGACAA	240
AATCCATGAC	ATGTCCACCG	AAGGTCAAAT	CATCTGATAT	GAAGTGCAGA	TGGTAGCCTG	300
CCACACTGAC	CCCATGGAAA	ATCTCAGGCG	TCCAGAAACC	AACAATAGTC	CCCAGCAACAT	360
TGTCACGACT	ATATTCCGGT	TGATGGGTTG	CGACATCAGC	AAACTTGGTA	TCGGGTGTTG	420
ACTTAGGAAT	CATACGCACA	TGCATATGTT	AAAAATTCCC	CCCCGAATCT	TGATAGAGCG	480
GAAAAGATTT	TCCCCATCAT	AATAAGACTC	AATTCGTTCT	TTCAATTCTT	TGTCTGTCAT	540
CTCAAAGCGC	TGGCGAAAAA	TGACCTCTGC	CTGATGCGGT	ACCACTGCAG	CGTAAGGAAT	600
AAGGGCATCT	GGTGACACTT	CCACAATTTT	TGGCTGGTCT	CCTGACCCTT	TGG	653

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 989 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTACGATATC	TTTGGTCTTT	TGTAAGATAT	GAGGTCCACC	CTTATGCGCC	TCAGTTGGCA	60
TTTCATGCGA	TTCAAGAAGT	TGCCCCCTCT	GATCAACCAA	ACCATACTTG	ATGTTGGTTC	120
CACCGATATC	AATTGCAACG	TAATATGTCA	TAAATACCTC	CTTTTAGATT	AGAGGAAGCG	180
CTCCTTGGTT	TCACGAATCA	AGGCAGCAGC	CGCTTCTACA	ACTGGACGAT	CTTCTTCAGT	240
CACTGGTGTC	AATGGTGAAC	GAACAGATCC	AATATTCAAG	CCTTCATTGA	TTTTCAGAC	300
TTCTTTGATG	ACACCGTACA	TATTTCCATG	AGCAGAAGTG	AGTTTACCAA	TGATTGCGTT	360
GATAGCATAC	TGCAATTCAC	GCGCTGTTTC	TAGGTCCTTA	TCCGCAATCA	ACTGATTGAG	420
TTTCAAGAAG	AGTTCTGGCA	TAGCACCATA	AGTACCACCG	ATACCAGCCC	TAGCCCCCAT	480
GAGGCGTCCT	CCTAGGAACT	GCTCATCAGG	ACCATTAAAG	ACGATATGGT	CTTCTCCACC	540
AAGGCTGACA	AAGGTTTGGA	TATCTTGAAC	TGGCATAGAA	GAGTTCTTCA	CACCGATAAC	600
ACGAGGATTT	TTCAACATTT	CTGTGTAAAG	GCTTGGAGTC	AAAGCAACCC	CTGCCAATTG	660
AGGAATGTTG	TAAATCACGT	AGTCTGTGTT	TGGAGCTGCA	GAAGTGATAT	CGTTCCAGTA	720
TTTGGAACCT	GAGTTATTCT	GGCAAGCGGA	AATAAATTGG	TGGAATCCGT	TGCAATAGCA	780
TCTACTCCCA	AGCTTTCAGC	ATGGCGAGCA	AGTTCCATAC	TATCTTTAGT	ATTATTGCAA	840
GCAACATGGG	CAATAATGGT	CAATTTACCT	TTGGCTACCG	CCATGACTTC	TTCCAAAATC	900
AACTTGCGAT	CTTCAACGCT	TTGGTAGATA	CATTCACCAG	AAGAACCATT	GACATAAGAC	960
CTTGAACACC	TTTATCAATG	AAGTATTGA				989

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1671 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TCAAAGAGTA	ACAAAGGCAC	CAAATTCTCG	ATAGGAACGA	TTTAGCACGG	TAAACTTCAT	60
CCACTTGGGT	TCACGGAACC	AAACCAGCAA	TAATTTCTTT	GGGCACGGGT	TAATAGCATT	120
TTGGTCAACT	AGGAGTAGAT	AGAACACATT	TCNTTCTTCG	TCTATATCAA	TCTTAACACC	180
TGTTTCAGCG	ATAATCTTGT	CGATGGTTTC	TCCACCCTTA	CCGATGACAA	TCTTAATCTT	240
GTCCACATCA	ATCTTGATCG	TATCAATTTT	CGGAGCAGTT	GGAGCCAATT	CTGGACGAAC	300
TTCTGGAATG	GTTGCTTCAA	TGACATCAAG	GATTTCAAAA	CGCGCTTTCT	TGGCTTGAGC	360
AAGAGCCTCC	GTCAAGATTT	CTGCAGTAAT	CCCTTGAATC	TTGATATCCA	TTTGAAGGGC	420
TGTAATCCCA	TCACGAGTAC	CTGCAACCTT	GAAGTCCATA	TCTCCAAAGT	GATCTTCCAA	480
ACCTTGATA	TCTGTCAATA	CTGTGTAGTT	ATTTCCATCT	GAGATAAGTC	CCATAGCAAT	540
ACCAGCTACT	GGCGCCTTGA	TTGGCACACC	ACCAGCCATA	AGGGCAAGAG	TTCCCGCACA	600
GATAGAAGCT	TGAGATGAAG	AACCGTTTGA	TTCCAAAAC	TCTGCTACTA	GACGGATAGC	660

GTATGGGAAT	TCTTCCAAGC	TTGGCAAGAC	TTGAGCAAGA	GCACGCTCAC	CAAGGGCACC	720
GTGACCGATT	TCACGACGAC	CTGGCGCACC	GTAACGACCT	GTTTCCCCTA	CAGAATATTG	780
AGGGAAGTTA	TAGTGGTGCA	TAAAGCGTTT	CTTGTACTCT	GGATCCAAAC	CATCAATGAT	840
TTGAGTTTCT	CCCATCGGAG	CCAAGGTCAA	GACTGAAAGA	GCTTGAGTTT	GCCCACGAGT	900
AAAGAGACCT	GAACCATGTT	ACACGAGGAA	GGAAGTCAAC	AACCGCATCC	AAAGGACGGA	960
TTTCATCGAC	CTTACGACCA	TCAGGACGCA	CCTTGTCTTC	TGTAATTAAA	CGTCGCACTT	1020
CTGCGTGTTT	CATTTGTTCC	AAGATTTTCA	CCACATCACG	CATAATACGG	TCAAATTCTT	1080
CGTGGTCCGC	ATATTTTTCT	TCGTAAACGG	CAGTCACTTG	GTCTTTCACT	GCTTGAGTTG	1140
CAGTTCACGG	GAATCCAATT	TCTCTTCTAC	TTGAACTGCC	TTTTGGAGGT	CAGTGTGTGA	1200
GGCTGCAATG	ATTTCAGCTT	GCAATTCAGC	ATCCACGTGA	AGCAATTCCA	CTTCTGCTTT	1260
TTCTTTACCG	ACAGCAGCAA	CGATTTCTTC	TTGGAAGGCA	ATCAATTCTT	TGACAGCTTC	1320
GTGCCCTTTA	AGAAGCGCTT	CCAACATGAT	TTCTTCTGAC	AATTCTTTGG	CACCAGACTC	1380
TACCATGTTG	ATAGCGTGCT	TGGTTCCAGC	TACTGTCAAT	TCAAGAAGAG	ATTGCTCTGC	1440
TTGTTCTTGA	CTTGGGTGTA	TGATGATTTG	GCCATCTACA	TATCCCACTT	GTACCCAGC	1500
AATTGGTCCG	TCAAATGGAA	TATCTGAAAT	AGACAGTGCC	AAAGATGAAC	CAAACATAGC	1560
AGCCATTGGT	GCAGATGCAT	TTTCATCATA	AGAAAGCACT	GTATTGATGA	CTTGGACTTC	1620
ATTACGGA	AA	CCTCCGCAA	ACATAGGACG	AATCGGACGG	TCAATCAAAC	1671

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTCAGTATCT	TTGTAATCAA	CATATCCAAT	TTTGTGTTGCT	GCGATGTANT	CAACTTTTTTT	60
ACGGCGTTTG	AATCCGCCAC	GACGTNGTTG	AGCCATGTTT	TTNCTCCTTT	ATAAGTTTAG	120
TTGTCCATTA	GAATGGTAAA	TCATCANCTG	AAATATCCAA	TGGGTTTGTT	GCTCCAAATG	180
GATTTTCATT	ACGTGAAAAG	TCTGGTACTG	AATTTGTAGG	TGCTGAATAG	TTTGCAGTTG	240
GTGCAGAGTA	AGCTCCACCT	GTGTGACCCT	CACGCACACT	ACGGCTTTCC	AACATTTGGA	300
AATTCTCAGC	CACGACCTCT	GTCACGTAGA	CACGTTGTCC	TTGCTGGTTA	TCGTAACCTAC	360
GAGTCTGGAT	ACGACCTGTC	ACCCCGATAA	GTGAGCCTTT	TTTAGCCCAG	TTAGCAAGAT	420
TTTCAGCCTG	TTGGCGCCAC	ATAACGACAT	TAATAAAATC	AGCCTCACGT	TCACCATTTT	480
GACTCTTAAA	TGTACGTTT	ACTGCAAGAG	TAAAAGTCGC	AACTGCTACA	TTTGATGGGG	540
TATAACGCAA	CTCAGCGTCA	CGTGTCTATC	GCCCTACAAG	TACAACATTG	TTAATCATAG	600
TTTACCTTCT	TACGCGTCAA	TTTGTGACGAT	CATGTGACGA	AGAATGTCAG	CGTTGATTTT	660
GGAAAGACGG	TCAAATCTTT	TAGAGAGCTG	CATCGNTCAT	TTGCTTCAAC	GTTAACGATG	720
TGGTAAAGTC	C					731

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 992 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

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CTGGGTTTTTA CCACGTTTTC CTGATGTACG AGCGAGATCC TTACGGTTCA ACATAGTGTT      60
GATAAAGCTG GATTTACCAA CATTTGAACG CCCTGCTAGG GCAATCTCTG GCAGTTCATC      120
CTGCGGATAG TGGGACTTAT TAGCTGCACT GAGCAAGATT TCAGCATTGT GTGTATTAAG      180
TTCCATAGTC ACCTCTAGGC TGTTTCTAGG ATCGGTTTAT CCGTTCCATC GACAGTTTCT      240
TTAGTGATGC GAACCAATTT CACATTTTCC TGACTCGGCA CCTCAAACAT AACATCTAGC      300
ATGGTTTCTT CGATGATGGA GCGAAGTCCA CGCGCCCCTG TCTTCCGTTT GATTGCTTTA      360
TTAGCAATCT CTTGAAGGGC TTCGTCGTCA AATTCCAACCT CAACATCATC ATAAGAAAGC      420
AAGGTTTGGT ATTGTTTCAC CAAGGCATTT CTTGGCTCTT TCAAGATGCG AACCAAGTCC      480
ATCAACGGAC AATTGCTCAA GAGCCGCAA AACAGGCAAG CGTCCAATCA ACTCAGGGAT      540
AATACCAAAT TTTTGAATGT CTTCAGCGAT GAATTCTTGC ATGTATGAGC TGTTTCTCTG      600
TCAATCGCCT TATTGTTTTG ACCAAATCCG ATGACTTTTTT CACCCAGACG TTGTTTGACA      660
ATTTCTTCAA TACCATCAAA AGCACCACCC ACGATGAAGA GGATATTTTT TGTATCCACT      720
TGAATCATCT ACTTGTTGTG GATGTTTGCG TCCACCTTGA GGCGGCACGC TAGCAACAGT      780
TCCCTCAATA ATCTTGAGAA GGGCTTGTTG CACCCCTTCA CCAGAAACAT CACGTGTGAT      840
AGACACATTC TCACTCTTCT TGGCAATCTT GTCAATTTC TCCACATAGA TAATGCCACG      900
CTCTGCACGT TCGATGTTAA AGTCAGCAAC CTGCAAGAGT TTGAGGAGTA TATTTTCCAC      960
ATCCTCACCC ACATAACCAG CCTCCGTCAG AG                                         992

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(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

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ATTTTCACAG GGCAGGATGC GGAACGACTA GCCCCATACT TTAACGGAAT TTTGGTAGGG      60
ACAGCTCTTA TGCAGGCAGA AAATGTGGCC CAGAGAATCA AGGAGTTGCA GATTGACAAA      120

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GGTTAAAATT	TGTGGACTAT	CGACCAAAGA	AGCGGTGGAA	ACAGCCGTTT	CAGCAGGAGC	180
CGACTATATC	GGTTTTGTCT	TTGCACCTAG	TAAAAGACAG	GTGACTTTAG	AAGAGGCAGC	240
TGAGTTGGCA	AAGCTTATTC	CTGCAGATGT	GAAAAAGGTT	GGAGTATTTG	TTTCACCAAG	300
TCGGGTAGAA	CTGCTGGAAG	CGATTGACAA	AGTTGGCTTG	GACTTGGTTC	AAGTTCACGG	360
TCAGGTGGCA	GATGATTTAT	TTGAGAATTT	GCCTTGTGCC	AGTATTCAGG	CTGTGCAGGT	420
AGATGGAAAT	GGGCATGTCC	CCAATTCTCA	GGCAGATTAT	CTACTCTTTG	ATGCCCCCTGT	480
GGCAGGAAGT	GGCCAGTCCT	TTGATTGGGG	TCAACTGGAT	ACGACTGGAC	TAGCACAGCC	540
CTTCTTTATC	GCAGGTGGCC	TTAATGAAGA	TAATGTAGTA	AAAGCAATTC	AACATTTTAC	600
TCCCTATGCA	GTAGATGTAT	CGAGCGGAGT	GGAGACAGAT	GGACAAAAAG	ATCATGAAAA	660
GATTAGAAGA	TTTATAGAGA	GGGTAAAGCA	TGGCATATCA	GGAACCAAAT	AAAGATGGAT	720
TTTACGGAAA	ATTCGGCGGA	CGTTTTGTCC	CAGAAACATT	GATGACAGCA	GTTTTGGAGT	780
TGGAGAAGGC	CTACCGTGAA	AGTCAGGCAG	ACCCAAGTTT	CCAAGAGGAA	TTAAACCAAC	840
TCTTGCGCCA	GTACGTAGGA	CGTGAAACTC	CTCTTTACTA	CGCAAAAAAC	TTGACCCAGC	900
ATATCGGCGG	AGCCAAGATT	TATCTCAAAC	GGGAAGACCT	TAACCATACA	GGAGCCCACA	960
AGATTAACAA	TGCCTTAGGA	CAAGTTTGCC	TTGCCAAACG	CATGGGTAAA	AAGAAAATTA	1020
TCGCAGAAAC	GGGTGCTGGT	CAGCACGGTG	TGGCAACTGC	AACTGCTGCG	GCCCTCTTTA	1080
ACATGGAATG	TACCATCTAC	ATGGGTGAGG	AAGATGTCAA	ACGCCAAGCC	CTCAATGTGT	1140
TCCGTATGGA	GCTTTTGGA	GCTAAGGTTG	AAGCAGTGAC	AGATGGTTTCG	CGCCTGCTCA	1200
AGGATGCGGT	CAATGCAGCC	CTTCGTTTAT	GGGTGGCTAA	TATCGACGAT	ACCCACTATA	1260
TCCTTGTTTC	TGCCTTGGGG	CCTCATCCAT	TTCCAGAAA			1299

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1078 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CTGTTGAATC	AACAACACGT	ATCCAAGTAT	CAGNATCAAA	TTATGCAGGT	AATCGTACAA	60
TTGGAAATCA	CCGTGGATGG	TTCAATCCAA	CAACAACCTC	TGAAGGTTTT	GTTACATATA	120
TTTATGCAGA	TTAATTTACA	GAGGGACTCG	AATAGAGCCC	TCTTTTCAGG	TTTTACCGTG	180
ACAATCCCTA	TTAAAAATTA	TATCAAAATA	GCTTGAAAAT	ATTGGAAAAAG	TATGGTAGAA	240
TGAAAAATTGT	CGTGTGAACG	ATAATACTCA	TTCTTGATGA	ATTGTGAAGC	AGTTGCCCTT	300
GGGTCGTTTT	GCGAGTTGAA	GTCAAGAAGA	GGAAAAAAAC	AAAAAGGAGA	AATACTCATG	360
GCAGTAATTT	CAATGAAACA	ACTTCTTGAG	GCTGGTGTAC	ACTTTGGTCA	CCAACTCGT	420
CGCTGGAATC	CTAAGATGGC	TAAGTACATC	TTTACTGAAC	GTAACGGAAT	CCACGTTATC	480
GACTTGCAAC	AAACTGTAAA	ATACGCTGAC	CAAGCATACN	ACTTCATGCG	TGATGCAGCA	540
GCTAACGATG	CAGTTGTATT	GTTTCGTTGGT	ACTAAGAAAA	CAAGCAGCTG	ATGCAGTTGC	600
TGAAGAAGCA	GTACGTTTCA	GTCAATACTT	CATCAACCAC	CGTTGGTTGG	GTGGAACCTC	660

TACAAACTGG	GGAACAATCC	AAAAACGTAT	CGCTCGTTTG	AAAGAAATTA	AACGTGGATG	720
GAAGAAGATG	GAACTTTCGA	AGTTCTTCCT	AAGAAAGAAG	TTGCACTTCT	TAACAAACAA	780
CGTGCGCGTC	TTGAAAAATT	CTTGGGCGGT	ATCCGAAGAT	ATGCCTCGTA	CCCCAGATGT	840
GATGTACGTA	GTTGACCCAC	ATAAAGAGCA	AATCGCATGT	TAAAGAAGCT	AAAAAATTGG	900
GAATCCAGT	TGTAGCGATG	GTTGACACCA	ATACTGATCC	AGATGATATC	GATGTAATCA	960
TCCCAGCTAA	CGATGACGCT	ATCCGTGCTG	TTAAATTGAT	CACAGCTAAA	TTGGCTGACG	1020
CTATTATCGA	AGGACGTCAA	GGTGAGGATG	CAGTAGCCGT	TTGAAGCAGA	ATTTGCAG	1078

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CTATGAGGGA	TATAAAGTGA	GAGAGTTGGG	CCAACGTTCC	AAAAACGTCC	TAAATTCTGC	60
CCATTGACAA	AGGCAACCCC	CTTACCAAAC	TCAGACNAGT	CTAGGTAAGT	ATCTTTTGGC	120
TATTCGACTG	TAAAGTCATA	AGCGTAAAG	GCTGGTTGTC	CTTGAGTCCA	TCCTTTGGAA	180
AAATCAATTT	TCTCAGGATT	GTCTAGTGGG	AGTGGATAGT	GTTTCCAGTT	TAGTAAGAAA	240
TGCAGATCCT	TACAGACCCC	TGTCCGAATT	CCCTTACGTT	GCGTATCCGC	TAAGAACTTA	300
TGCCCATAGT	TGACACGCCC	CATATTTTCT	ATCAAGATAT	CTAACCTAGA	TAGCCCTTTC	360
TTTTTACCTT	GATAAAAAAT	ATCTTCCCCA	ATCTCTGTCT	GATATTGAGT	TTTAACCCAC	420
TGACCATCGA	CATACAGCTG	GGCCCTATCT	CGACCATCAA	TGATACGAAG	TCTTTCTTCT	480
TCTGCATCCC	AGTTTGTTTC	TGTTGATAA	AGTAGGTAGC	CATAACTTTG	TCCCAGCTCC	540
TCCATCTTTT	GAGGATAGAG	ACTTTCTACA	GGGACTTGAC	AAGCTATCTA	AGGTTTCAAA	600
CAAAGAACT	TTTTCAACTA	GTGGAATAGC	ATCCAACCTC	ATACTCTCTT	TGTAGAGTGG	660
TTCCAACCTG	GGATACTCTG	AAAAATGTGT	TGCCATCATC	TTCTTGACTG	CAAGATATTT	720
AGCAGTTGGA	TTTCCTTCTT	CATCCAGAAG	GGCATCGTAA	TCATAAGACG	TTAACTTGTG	780
GCAGGTCCAA	ATTCCTCGAG					800

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 769 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CTCACGCAGT	TCTGTTACCA	AAGACCGTTC	AAAAAGCAAA	CTAGCAATAC	TTATAACTTA	60
TTAGAAATTC	CTAATTTTAC	CTTGCTAAAC	GAATACAGGT	CACGATGCCA	TCTGAGTCTG	120
TGATTTCCAA	TTGGCTCGAT	GTCATCCATT	TGATTGGTAC	GTCAACTTCT	TGTGCTCGTT	180
GGGCAATCGT	TAACAGTTCT	TCTTTATGTG	CAACTTCGAT	GACATAGTAG	GCTAAACCTG	240
GTAAGCCTTG	CTTACGCGGA	AGCCAGACCT	TTTCCTTCCC	CATTTCGTAA	CTGCTAAATG	300
ATGATGGTAA	TCTCCAGCCG	CAATCCAAC	AGCGCCAGGC	ACACTGAATT	TATTCTCTAG	360
CCCTAACACC	TTTGTATAAA	ACTGGCTGGA	CTTTCGACTA	TCCTTGACGG	AAAGATGAAT	420
ATGCCCCATT	CTTGTAACCT	CTGCCAGGAT	AAAGGGCTCT	ACTCTTTCCC	CCAACTCATA	480
AATGTCCCTG	GCCGCAAGAG	CCTCCGTCAC	TCCGATAATG	CGTCCATCTT	CTCGAATATC	540
CCATGTGGAA	ACTGGCTTAT	CTCGATAGAG	TTCAATGCCA	TTTCCCTCCA	AATCTTCCAA	600
GTAAATAGCT	TCACTGTAAC	CATGGTCTGC	ACCGCCGACA	AGAGGAATTT	GCAAATCTGT	660
CAGATGTTTC	AAGACATCAG	CCAAAGCCTT	GCGTGTGGGC	AAGAGAATGG	CCAAATGGTA	720
AAGACCATAA	TGTTCCCTCA	CTTCTCCGCT	CTTCTTGTGC	TTGAATCAG		769

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TTACCCCAAG	CCTGCAACTT	CCCAAGCTGA	TTGGTTGAAT	GATTTGTCAT	CAACACCACC	60
AGTATCAGTG	ACGATTGCTG	CTTTTGTCTT	CACATCAGAA	GATGAAGCTG	CGTTACGAGA	120
AGAGCGGTTA	CCACATGCAG	CAAGTCCAAC	TGCTGCCACT	GCAACTAGGC	CAAGACCTAG	180
CCATTGTTTC	TTGTTCATTA	CTGAACCTCC	TAAATAAGAT	GTGCAACGAT	GTTGCAAGTA	240
TGGATTGATT	GGTCACAAAG	ACCCTTGCCA	CTCAAAGAGC	GA CTCAGACT	AATTTAAGTC	300
TGTAAAAGAA	TATGGAAGTA	ACTCCCCGAC	CGTCATCTCG	ACCGTCGATT	TATCTTTTGC	360
GACTAAGGTC	ACTTTTAAAT	CTTGTTCAAA	AAATTCGACC	ATTACTTGGC	GACAAGCACC	420
ACATGGTGAA	ATCGGTTTTT	CAGTTTGACC	ATAGACAATC	AATTCTGAAA	ATTCTCTTTG	480
GCCTTCAGAT	ATAGCCTTAA	AAATAGCTGT	TCTCTCACCG	CAATTGGTCC	AAAGGATAGC	540
TAGCATTTTC	GATATTCACT	CCCGTGTTAA	ACATTTCCGT	CTTTGGCTAC	TAAAAC TGCT	600
CCGATAGGAA	AGTGAGAATA	GGGGACATAG	GCATGTT			637

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 940 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CTGAGGATAA	TGACATCTGC	CANAGGAGCA	AAACTAGCAA	AATCATCNGT	TGCACGGTCA	60
ATCATGCCTT	CTTTCAAGGC	GATATCTCTC	GAAGCTTGAC	TACGGATTAT	AACCTAAAAT	120
TTCATAATCT	GGATGATCGC	GTTTGATACC	AAGTGCCATA	GAGGCTCCAA	TCAACCCAAG	180
ACCTGCGATA	TAGATTGTTT	TTGCCATAGG	AACTCCTTAA	TAGTTCTTTG	TATAGTCTCG	240
GTGTTTGGCT	ACCGCTTCTT	TTAGTTCCTC	AAGATTATCT	GATGAGAATT	TTTCGAGGAT	300
TTCTTGCGCC	AGAACC GTTG	CTACAAC TGC	TTCCATGACC	ATTCTCTGAG	CTGGAAGAGC	360
AGTCGGATCA	CTTCTCTCCA	CGGTTGCCTT	GTAAGGTTTCG	TGGGTTTTCGA	TATCCACACT	420
CATAAGAGGT	TTATAAAGAG	TAGGAATGGG	TTTCATGACC	CCACGAACAA	CGATGGGTTG	480
CCCATTAGTC	ATACCACCTT	CAAAACCACC	TAGATTATTG	GTACGGCGAG	TATAACCGTC	540
TTCTTTAGAC	CAGAGAATTT	CATCCATAAC	TTGGCTGCCT	TTACGATAAC	CAGCCTCAAA	600
GCCAAGACCA	AATTCACCCC	CTTTAAAGGC	ATTGATAGAG	ACAACAGCTT	GAGCCAATCT	660
TGCATCCAAT	TTTCTATCCC	ATTGGGACAT	AGGAACCAAG	ACCAACTGGG	AACGCCTCCG	720
ACGACTGTCT	CCACAACCCC	ACCGATGGTA	TCACCATCAC	GTTTGATTTG	GTCAATATAG	780
TCCTTGATTT	CCTGTTCTCG	TTCTTGGTTG	ACAATAGAAA	ACTTCCAGAC	TGGGCAGCTC	840
TTTGCTTTAA	TTTCCAGCGA	CTGTCAGATT	TTCCAGGAAC	ATCCATTCCC	TTGCCACCAA	900
AGACCACGAC	ATGGTTGGCA	ATCTCCATAT	CCAGATTTCGA			940

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GATTCTACAG	GATCCATTTT	ACTATCTTAC	GCGCCGGGAA	GTAGGCTGAG	ACATAACCAA	60
GTAATAGAGC	CAACAACTAG	AGTTCCTAAA	ACAGATAAAA	GATTTAATTC	AAAAACCTTA	120
GTGATGGATG	GGTAAAAGTG	ACTTACAATC	GCATTCGCCA	AACTTCCCAC	CCCTTG TGCA	180
ACCAAAAATG	CCAGCAGCAA	GGCGATGCCT	ACAATCCAGA	TAGCCTCGTA	AATAAAAATT	240
CCTTTGACAT	CACGATTCTG	ATAACCAACT	GCTTTTCATGA	CACCTATTTC	CTTGGAACGT	300
TGCATGATAT	TGATGTAAAT	AATGATACCA	ATCATAACCG	CTGCTACCAC	AATAGCTTGT	360

GATGAAAGCA CAATCAATAA TCCCTGAATA ACACGAATAA AGGTAATCAC AATATCAAGA	420
ACTCTCTGTT AAGAAAGCAC AGTATACTTC TTATTTTCT GTAAATCTTC TGTTACTACT	480
TTTGTCTGTG ATGGATCTTT GAGTTCCAAG ATAAAAATAAG ATACAGCTTT CGTAAATCCA	540
GCCTCTTTCA AAATCGTTTC CATTTGATGA GACAGCATGA AACTGTTGCT GTCCTCCATG	600
TCATCTTCAT CATTGATTAC ACGTACAATC TTCGTTTGAA ATTGAGCAAT CTTACTAGTT	660
TCGGCAGCAC TTTCTACAAT GCTGACTGAG ACTGATTTGC CAATAAGATC ATTAGCTGTC	720
AAATTTTTTC CTGTCTGTTT ATTCCAATTT TTTAGTAAAG CTGCTTGGA TCGTTAATCC	780
CTGTTCAATTT GTATCAGTAT AGAGGGATCC AGCCAACACT TTGTCCGTCT CATTATTACT	840
AACAGAGATA CTTGTATCAT CATAAAGACT CACTACTTGA GCATAAGAAG CATCGTTTGA	900
CTCAAATCCA TTTCTTGCCC ATCTTTTCTT GCCCATCTAT AGTAATATTT GACATGTTCA	960
TCCCNAAAGG ACTCTCCAA TATNNNATAG	990

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATCGGCTAAG ATGCGTGGAG CATCACAAAT TATCCTTATG AGCCGTCATG AAGACGTCAA	60
AAGATGGCTA TGGAGTCAGG TGCGACAGCT GTTGTTCAG AACGTGGTCA AGAACGAATT	120
ACCAAGGTGC GTGAAATCCT CGGCGGAGGA GCAGACGCAG CACTTGAATG TGTGTTGACG	180
GAGGCTGCTA TAGAACAGGC GCTAGGTGTT CTTCATAATG GAGGGCGTAT GGGCTTTGTA	240
GGAGTCCCAC ACTATAATAA TCGTGCTCTT GGTTCGACAT TTATGCAAAA TATCTCTGTA	300
GCAGGTGGGG CAGCTTCTGC TACAACATAC GATAAGCAAT TTTTACTAAA AGCCGTCCTT	360
GATGGTGATA TCAATCCAGG TCGCGTCTTT ACTTCAAGTT ATAACTGGA AGATATCGAC	420
CAAGCCTACA AAGATATGGA TGAACGTAAG ACCATTAAGT CTATGATTGT AATCGAATAA	480
AAAACGAATA GGAGTTTTAG AACTCTATTC GTTTTTTATG TTATCCTATT CTTGATTTAA	540
GGTACTTTCT CTTAATGTCA GTCTGGTTCC CAGCATGGTC AGGCTAGGGA TTTTCCGACC	600
GTGGAGGACT TCCTTGTTAA GAATATCCAT ACCTGCTCGG CCCATTTCTT CAGTATAAAC	660
TGTAATACTA AGAGAGGGGA GGATAGACCT GTTTGGTCAG ACTAAGTGTC GTTAAAAGGA	720
AAATGAGGCT GACGCGATCT GGCAGGCTGA TTCCAGCTTC TTGGAGGGCA CGGAGGGCAC	780
CGATAGCTAA ACTATCGCTG GCTGCGAAAA ATGCTGGCGG AAGTTGGTCT CCCAAGCTCT	840
GAATGGCCTC CTTCAATTAAG TCATAGCCAG ACTGGGCAGT AAATCTTCCT TGAAAGACCA	900
GTTTCATCATG ATAGATTCCC CTCGCTTGAC TGAGTTTTT GAAGTTTTCT AGACGCTTGT	960
CCTGAATGAT TTCTTCTTGG TCTGTAGTTT CTTCAAGGCC TGTAGAATC CCGATACGGT	1020
CCATTCCTTG ACTGAGGAAA TAATCGACAA CCTGTTTCAT AGCAGTGTA AAATCCGTGA	1080
TAATACAGGT ATGTCCCAGG GAAAGTGTAT CGCTGTCTAG AAATACAAGA GGCTTTTGGT	1140
ATTCTTCAAA GGCAGAAATC TGAGCTTCTT GATAGGATTG ATTCTGCTAG GGATAACAGC	1200

CAAAGGCAAT CCTCCCTTTA TCCACCTCAT ATTTGAAACC ATTCAGCTC TTA

1253

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CGTGTACCAT	CAAGAGGCTA	ATTGATGTTT	CTTCCCCCTG	TGCCTCTCTT	GTCAACATTT	60
CTGTTTGAGC	CTTATGCGCC	TGTAATAAGG	CAGCATTCGC	ATCAGCTAAT	CTTCGATTGG	120
CTTTAGAGAA	ATCCCCTTTT	TTTGCTGCCT	GAATAGCCTC	CATAGCATT	CTTTTGGCTT	180
CCCCACCATA	CATAATTAGC	CCCATTACAG	ATTCTAAATT	ACTTTCATCC	ATAACATTCT	240
CCTCAATCTT	AGTCTAATAA	ACTTTCAGCT	AAATCTAAGA	CTTTAGAACC	ATTCATCATT	300
CCATAATCTG	TCATCGGAAT	AACCGCCACA	GGAATCTGTC	TATCTTTTAG	TTTTTCTTGA	360
AAGTCCCCTA	GTAAATAGCG	AACTTGAGGA	CCTAAAAGCA	ACACATTTAC	TTCTTTTGTT	420
GCTACAATTT	CTTCTGCTTC	AGGAGCTGGA	ACTGCAAAAA	TTTCTGCATC	CAACCCCTTA	480
TCTTCTGCTG	CCTTTTGCAT	CTTTGTCACT	AGCAGACTTG	TACTCATACC	TGCTGCACAT	540
GCTAACATAA	TTGTTACTTT	AGCCATAGCT	TACTCCTTTA	TCACCTATTT	ACTGACCTAG	600
CCAAGCGAGA	TACTGTATGT	CTCACTCCTC	TAATTGCCTT	GCTCAATGCA	TAAATATTAT	660
CGACTGTTGC	CAGTCCCCCA	TATCCTGCGT	CACCTATATG	TTGAATATCA	ACTCCACAAA	720
TTTTATTTCT	AAGTGCAATT	TCCTTAATAG	TATCTGTATC	AGATGTTTCT	TGGCTAGTAC	780
CAATAGCACT	CAATACAAGA	CCACCCTTAC	TATGAACGAG	ATCAACGACT	TCACGCAACT	840
CTTGGTCATG	AAAGGCTGGA	ACGGTTCCAA	CTGCTGGAAC	AAGTATCACA	TCCGCACCTG	900
CTTCCAACAA	TTGCTCTGCG	ACAGAAAGCT	CTGCCACAGG	CTCATTCACT	CCTGCCCCGT	960
GCATCTTACC	TGCAATAATC	AAACCAGAAA	AGTTTTCCTT	AGCAGTTTGA	ACAGCCTTAA	1020
TGATTTCTCG	ATTGCTAACT	CCTGTTCCAG	GATTTCCAGT	CAAACAGACA	AAGTCAAAAC	1080
CTAACTCCTA	TATTCGCTTC	AATGTTTCAA	CACTAGCAAC	ACGACCTGCA	ACAATTTCTT	1140
GTGTTTCCTC	TAGCATTCTT	TGCAGATGGG	TCAATCGGTT	CCAAATTTAC	ACCAATTGGA	1200
CAAGCAACAA	G					1211

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CCACACTAGC	AGCCTATGGA	CTCACTAAAA	GAAAAGAAGA	CTAAGTCTTT	TCGATAAAAA	60
ATAAACAGCG	AGATTGAAGC	TCGCTGTTTA	TTTTTTAATT	AATCACCTAG	TCCAAGACGT	120
TCAAAGATAT	CATCCACTCG	TTTGGTGTA	TAAACTGGGT	TGAAGATTTC	ATCGATTTCT	180
TCTTGTGTGA	GACGTGATGT	TACTTCTGAA	TCTGCCTCAA	GAAGTGGTTT	AAAGTCTACT	240
TGGTTGTCCC	AAGAGTAGGC	TGTTTTTGGT	TGCACCAAGT	CATAGGCTTG	CTCACGGGTC	300
ATGCCTTTTT	CAATCAATGT	CAACATAGCC	CGTTGGCTAA	AGATAAGACC	AAAAGTCGAG	360
TTCATGTTTC	GGATCATATT	TTCTGGGAAG	ACTGTCAAGT	TCTTGACGAT	ATTTCCAAAA	420
CGGTTGAGCA	TGTAGTCAAT	CAAAATGGTC	GTATCTGGTG	TGATGATACG	CTCAGCTGAT	480
GAGTGAGAAA	TATCGCGTTC	GTGCCAGAGA	GCGACGTTTT	CATAAGCCGT	AATCATGTGA	540
CCACGAATGA	CACGCGCCAG	ACCAGTCATA	TTTTCAGAAC	CGATTGGGTT	GCGTTTGTGA	600
GGCATTGCTG	AAGACCCTTT	TTGCCCTTTA	GCAAAGAACT	CTTCTACTTC	GCGTTGCTCA	660
GATTTTGTGA	GACCACGAAT	CTCAGTCGCC	ATACGTTCTGA	TTGAAGTCGC	AATGCTGGCA	720
AGAACCGCAA	AGTACTCAGC	GTGAAGGTCA	CGAGGAAGGA	CTTGTGTTAA	AGATTCCTTG	780
GGCACGGATG	CCAAGTTTAT	CGCAGACATA	CTCCTCTACA	AATGGTGGA	TATTGGCAAA	840
GTCCCAACC	GCACCAGAAA	TCTTACCAGC	TTCTACACCA	GCAGCCGCAT	GCTCGAAGCG	900
CTCCGATATT	GCGTTTCATT	TCGCTGTACC	AAGTTGCTAA	TTTAAGGACC	AAAGGTTGTC	960
GGCTCAGCGT	GCACACCATG	AGTTACGCCC	CATCATGATG	GTGAACTTGT	GCTCCTTGGC	1020
TTGTCAGCGA	TGATATTAGT	GAAGTTTCA	AGGTCACGAC	GGATGATGTC	GTTGGCCTGC	1080
TTGTAGAGGT	AACCATAAGC	AGTATCCACC	ACGTCGGTAG	AAGTTAACCC	ATAGTGAACC	1140
CACTTGCGCT	CTTACCAAG	AGTCTCAGAA	ACCGCACGCG	TGAAAGCCAC	CACATCGTGG	1200
CGCGTCTCCT	GCTCAATTTT	CAAAATACGG	TCGATGTCAA	AGTCCGCCTT	CTTGCGAATC	1260
AAAGCCACAT	CTTCCTTAGG	GATTTCCCCA	ACTCAGCCCA	TGCCTCGTCA	GAGAGGATTT	1320
CCACCTCAAG	CCAAGCACGG	TATTTATTTT	CTTCACTCCA	AATATTCGCC	ATCTCAGGGC	1380
GAGAGTAACG	GTTGATCATG	TGTTAATTTT	TCCTTTCTTC	TTAAG		1425

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1124 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CTATTCTGAG	TATAAAGTTG	GCGGAGGCTG	GAAGTACGCT	CGTTATGAGG	TCATAAACTA	60
CTATACTGGA	GGTTATTAAT	CCTTAAAGAG	TGAGAAAAGG	AGGGCTGGAT	ATGTTAAATC	120
TTACTCATGT	TACCTTAAAA	ACGCGACAAG	TCATCTTGCA	AGATGCGGAT	TTTACCTTTA	180

AAAAGGGTAG	GATTTATGGC	CTTCTTGCTA	TCAATGGCTC	GGGAAAGACG	ACACTATTCC	240
GAGCTATGAG	CAAGTTGCTT	CCCCTTAGTA	GTGGACACAT	CGCAGTTCCT	CCTTCTTTGT	300
TTTATTATGA	GAGCGTTGAA	TGGCTGGATG	GAAACTTAAG	TGGGATGGAC	TACCTTCGTC	360
TCATAAAAAA	ACATCTGGAA	GTCAGACCTA	AACTTGAGAG	ATGAAATCGC	CTACTGGGAA	420
ATGGCTGACT	ATATCAGTCT	TCCCATCCGC	AAGTATTCCT	TAGGGATGAA	GCAACGCTTG	480
GTGATTGCTA	TGTATTTTCT	CAGTCAGGCC	AAATGCTGGC	TCATGGATGA	GATTACAAAT	540
GGCTTAGACG	AGTATTATAG	ACAGAAGTTT	TTTGATAGGC	TAGCACAAAT	CGATAGACAA	600
GAACAGCTGG	TTCTTTTAAG	TTCCCACTAT	AAGGAAGAGT	TGGTTGATAT	CTGCGATAGA	660
GTAAGTACCA	TTCATCAGGG	GCAGATAGAA	GAGGTTTAGT	TTATGAAAGA	TGTTAGTCTA	720
TTTTTATTGA	AAAAAGTTTT	CAAAAGTCGT	TTAAACTGGA	TTATCTTACT	TTTATTTGCA	780
TCTGTACTCG	GTGTTACCTT	TTATTTAAAT	AGTCAGACTG	CAAACCTCAGT	CAGCTTGGAG	840
AGAGAGTTGG	AAACTCGTCT	TGTAGACCGT	GAGAGAGTCA	TCAATGAAAA	TGAAGAGAAA	900
CTCTCCCAA	TGTCTGATAC	CAGCTCGGAG	GAATACCAGT	TTGCTAAAA	TAATTTAGAC	960
GTGCAAAAA	ATCTTTTGAC	GCGAAAGACA	GAAATTCTGA	CTTTATTAAA	AGAAGGGCGC	1020
TGGAAAGAGG	CCTACTATCT	GCAGTGGCAA	GATGAAGAGA	AGAATTATGA	ATTTGTATCA	1080
AATGACCCGA	CTGCTAGCTC	TGGCTTAAAA	ATGGGGGTTG	ACCG		1124

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1089 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CAGAGCAACT	TCGTCAAATC	TTCATAGGTG	AGGTAACCAA	TTGGAAAGAG	GTTGGTGGTA	60
AGGACTNACC	CATCTCTGTT	ATCAATCGGG	CAGCCGGCTC	TGGCTCTCGT	GCTACCTTTG	120
ATACTGTCAT	TATGGAAGGT	CAGTCTGCCA	TGCAAAGTCA	GGAGCAGGAT	TCAAATGGAG	180
CGGTAAAATC	AATCGTATCA	AACAAGTCCA	GGAGCTATCT	CTTATTTATC	TCTTACCTAT	240
ATAGATGATT	CGGTCAAAG	CATGAAGTTG	AATGGCTATG	ACTTAAGTCC	AGAAAAATATA	300
AGTAGCAATA	ATTGACCCTT	GTGGTCTTAT	GAGCATATGT	ATACATTGGG	GCAGCCCAAT	360
GAGTTGGCTG	CAGAATTTCT	CAATTTTGTT	CTCTCGGATG	AGACCCAAGA	AGGGATTGTC	420
AAAGGATTGA	AGTATATTCC	GATTAAGGAA	ATGAAGGTTG	AAAAAGATGC	TGCCGGAAC	480
GTGACAGTGT	TGGAAGGGAG	ACAATAATGA	ATCAAGAAGA	ATTAGCTAAG	AAAATGTTGC	540
TTCCATCAAA	GAATTCTCGT	CTGGAGAAAT	TAGGAAAAGG	TTTGACCTTT	GCCTGTCTTT	600
CTTTGATAGT	CATCCTTG TG	GCCATGATTT	TGGTTTTCGT	AGCGCAAAAA	GGCTTGTCGA	660
CCTTCTTTGT	CAATGGTGTG	AATATCTTTG	ACTTTCTTTT	GGGAGGAACT	TGGAATCCTT	720
CTAGTAAAGA	ATTTGGTGCC	CTTCCTATGA	TTTTGGGTTC	CTTTATCGTT	ACCATTCTCT	780
CAGCCCTTAT	CGCAACACCC	TTTGCTATTG	GTGCAGCAGT	TTTTATGACC	GAAGTATCAC	840
CAAAAGGGGC	GAAGATTTTG	CAACCAGCTA	TTGAACCTCT	GGTTGGGATT	CCTTCAGTAG	900

TGTACGGATT TATTGGCTTG CAAGTCGTCG TTCCCTTTGT TCGCAGTGTC TTTGGTGGGA	960
CTGGTTTTGG GATTTTGTCA GGGATTTCG TCCTCTTTGT CATGATTTTG CCGACCGTAA	1020
CCTTTATGAC AACGGATAGC TTGCGTGCGG TTCCTCCTT ATTATCGTGA AGCCAGTTTC	1080
GCTATGGGA	1089

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CTNTNTTTAA ACCTTGACCT TANTTGANNA TTATACCGAA ATTNTCTTCA TTTTAAAAG	60
AAAAAAGGGC GCTGGTAAAA GGGATAATCT TCACCAACTC CCTATNTTTC TACTTATCTA	120
AGCCTAATTC TGCCAAGATT TGACGTTTGT NGGCAATCTT TNGGACTTCN TNGTCCTCAT	180
CTTCAGACCA GTCTAGTTTA ATTTCTGAAA CAATCTGCCC AGGGNGATTT NTCAAGATAT	240
AGATGCGGTC GCTGAGANTG AGGGCCTCCT CAATACTATG CGTGANGATC AGGGTTGTTA	300
GCTGCAACTG CTTGTGAATC TCAAGATACC AAGCGTGGAG TTCCATCTTT GTCATCTCAT	360
CCAAGGCGCT AAAGGCCTCA TCTAAGAGAA AGAGCTTGTG CCCAAAAAGG TAGGTCCGGA	420
GTAAGGCTAC ACGCTGGCGC ATCCCACCGC TAAGTTCATG AGGATACTTG TCTCTTACAG	480
CTGTCAGCTG GAAGGTCGCA AGAATTTTAT CCGCTCGGGA AATAGCTTCT GCCTTATCCA	540
CCTTTTGAAT CAAGAGGGGC AGAATGATAT TTCCAAGCAC CGTCTTGTCG TCCAAGAGCA	600
GATCCTTTTG CAACATATAA CTCACGTGCC CTTGGGATT TTCTTCACCA TCAAGGACAA	660
TTCTCCCTGA CTGAACTTCT AAAATCCAG CGATTAGATT AAAGAGGGTG GTCTTTCCAA	720
CACCACTTGG GCCTAGGATG GAAACCACTT CGCCTGAAGT CACCTGTAGG TTGATATCCT	780
CTAAAATCCT CTCCTGACCA TAGGCATAAC TGACGTGCTC TAGTCTAATT TCTGTCAATTA	840
TTTCACAAAT TCGTTGGTGA AGCCTTTGTC TGTCAAGTCT TCTTTAAGGA TACCATTTTC	900
TTTATCCCAT TTATAGAAAG CATTCAGCG AGCTGCGTCA AATTGACCCC ATTTTTCCTT	960
GTCGCTTGCG TATTCTTTTG ACAAGTATTT TTGAGATTCG ATGACAAAGT CACGTTTTTC	1020
CTTGAGTTCA GGTGCATTCT TGATGAGAAT ATCTGCAGCT TCTNCTGGAT GTTCCATGGC	1080
ATATTGGTAG CCTTTTNTGA TGGCTTGAT GACTTTGCGA GCTTCTTCTT TGTTATCTTT	1140
CAGATAGTCG TTGTTTGC GA TGATAACTGG TGAATATTAN TCAAACCTCCT TGACATAGTC	1200
TTTCAANTAC ATGAAGTTAG CATCTACACC TTGAGATTTA GCAAGGATAC CATCCCAACC	1260
GTAATAATC CNAGCAGTAT CAAAGACGCC ATTGGCAATC GGTGTGATTG AGTTTGAGTC	1320
NTTANTTGGT ACTNTTTC AA CCTTCTCACA GTCTCCNCCT TGAGATTCTA CCAAGGTTTT	1380
CAACATACNN GTTCANTTGG GTCATTCCAT GTCCCATATT TCTTACCAAC CAAGTCTTTT	1440
GGACTGCCTA CATNTTCACA TTACCGAGAG ATGATCCCTG ATGTATTGTG TTCCACCNA	1500
AG	1502

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1022 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

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ACTCTTCAGC GATTTCTTGG CTGAGAATGT CCTCATAGGC AGGGAGTTGG ATGTCCTGAC      60
CATATTTCTT CTTGAGGGCA GTAGTAACTA GGCGATAAGC CAGATTGGCA TTACGAGAGA      120
AGATAGGCCC GNGGAANTAC GAACCAAAGA CATTCTTATA ATGAACCCCT TCACCGACCT      180
TTTCTTCGTT GTTTCCATTT CCATAGACAA CCTGTCCCAG CGGTTTTTTGG TCATCAGAGA      240
GGAAGGTACG ACCTTGGTGA TTTTCAAATC CATAGTAGGT TTCATCGAAA TCTTTCATTG      300
TGAATCTTGA TGTCACCGAT AAAACGGTTA TTGGTCTGGT TGAGCGTGTA GTGTCCCATG      360
ACCCCTAGCC CTTGATACG TTTTCTGAA GCTTCAACAT AATATTGACC CAATAGTTGG      420
AAACCACCGC AGATAGCCAG AACTACACCG TCGTTTGGGA TGTAGTTGTC AATGCTCTCT      480
TTTTTAGCAG GTAGGTCGTC TGCAATGATA CTTTGTTCAG AGTCTTGACC ACCACCGAAA      540
AAGGCGATGT CGTAGTGATT TTCATCAAAG TCATCATGGA GAGAAACGAT GTCAACGGTC      600
ACATGGGTTT CCAGTTTTTC AGCCACATAC TTGAGCATGA GGATGTTTCC ATTGTCCCCG      660
TAGGTATTCA TGAGATTTC GTAGAGGTGG GCAATGTTGA GCTGATAGGG GTAATTGCCA      720
TCTTTTGAGG AAAGTGAAGT ATAAACCATT AGTTCATCTC CTTTCTAACA ATCTGACGAC      780
TAGCCAGCAG TTCACGAAAT TCCAGCATGG CAGTATAAGT TGCCAGAATA TAGGCATGCT      840
TGCAGTCTTG ATTCTCAATG GTCTTGAGAA CTTGCTCCAG ATTACTCGTT TCAGTGATTT      900
TCTCAGCTGG ATAGCCAGTC ACTCGGAGGC GACGAGCGAT TTCAGAATGA CGAACACCGC      960
CAGCGTTGAT TTCAGGAATG TCCATGTCAG TGATTGCTC AAAGTCTGCA TCCCAGATCC     1020
AG                                                                    1022

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(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

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CCTCCAGGTC TCGGGAAACG ACCATGGCCT TTGTTATTGC CAACGAACTG GGAGTCAATC      60

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TTAAGCAGAC	GTCGGGTCCA	GTCATTGAAA	AAGCCGGAGA	TCTGGTAGCT	ATTTTGAATG	120
AGTTAGATCC	TGGGGATGTA	CTTTTATTG	ATGAGATCCA	TCGTTTGCCA	ATGTCAGTGG	180
AAGAGGTGCT	TTATAGTGCT	ATGGAGGACT	TCTACATAGA	TATTATGATT	GGGGCTGGTG	240
AGGGTAGTCG	TAGTGTTTAT	TTGGAGTTAC	CACCTTTTAC	CTTGATTGGT	GCGACGACTC	300
GGGCTGGTAT	GCTCTCCAAT	CCGCTACGGG	CACGTTTTGG	GATTACAGGC	CATATGGAGT	360
ATTATGCCCA	TGCTGACTTG	ACAGAAATTG	TCGAGCGGAC	GGCAGATATT	TTTGAGATGG	420
AAATCACTCA	TGAGGCAGCA	TCTGAGTTGG	CCCTACGTAG	TCGTGGGACC	CCTCGTATTG	480
CCAATCGTCT	CCTCAAGCGC	GTGCGCGATT	TTGCCCAGAT	AATGGGGAAT	GGGGTAATTG	540
ATGATATTAT	TACCGATAAG	GCTTTGACTA	TGCTGGATGT	TGACCATGAA	GGTTTGGACT	600
ATGTGGATCA	AAAAATCCTT	CGTACCATGA	TTGAGATGTA	CAGTGGAGGA	CCTGTTGGTC	660
TAGGAACTCT	TTCTGTTGAA	TATCGCCGAA	GAACGTGAGA	CAGTTGAAGA	TATGTATGAG	720
CCTTACTTTG	ATTCAAAAAG	GTTTTATCCA	TGCGGACACC	GTCCTGGACG	GGTGGCGACT	780
GCCTAAGGCA	TATGAGCACT	TAGGTTATGA	ATACAGTGAA	AAATAAGCAA	GAAATCCTTA	840
GAGGCTTTTT	AGAGAAAATC	CAGATATGAT	GGCCATTCTG	ACGATCATCC	GAGACCTTGG	900
TCTGAAAGAC	TCGTGGTTGG	CAGCAGGTTT	TGTCAGAAAT	TTCATTTGGA	ATCTTTTGTC	960
AGACAAATCC	CCTTTTGATC	ATGAAACAGA	TATAGATGTT	GATTTTCTTT	GATCCCAGAT	1020
TTTTCTTATG	AGGAAACCTT	ATTACTGGAG	AAAAAGCTGT	GAGAGGATTT	TCCTCAGTAC	1080
CAGTGGGAAT	TGAAAAATCA	GGTCTATATG	CATCAGCACA	GTCCTCACAC	TGCTTCCTAT	1140
ACCAGTTCTC	GTGATGCTAT	GAGTAAGTAT	CCAGAACGGT	GTACGACAGT	TGGACTGCGC	1200
TTGAATGAAG	AATCAGATTT	TGAACTCTAT	GCACCTTATG	GTTTGGAGGA	TATTTTGAAT	1260
TTCAAGTTCG	TCCAACCTCT	CATTTCTTAG	AAAATGAAGA	CCGAATGGAA	CTCTATCAAA	1320
CACGTTTATC	CAAGAAAAAT	TGGCAGGAGA	AAT			1353

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CTCCTGGA	TTCTGGCAAG	TAGGCTGGAT	GAATGTTGAC	AATCCGACCT	TCATAAGCCG	60
ACAATAAGGT	TGGTCCAACG	ATTTTCATGT	AGCCTGCTAG	GCAAACCAAG	TCAATCTGGT	120
GTTCTTCCAA	GAGTTCGACA	AGGGCTGCTT	CGTAGTCTGT	CTTGCTCTCA	AACTCCTTGA	180
GTTCAAAAGC	ATAGGACAGA	ACGCCGAGCT	GCTTTGCACG	CTCAAGCACA	TAGGCATCAC	240
GATGGTCTGA	AAAGACAAAC	TCCACTGGAA	ATTCTTCGGC	AATCACCTGA	AAATTTGAGC	300
CATTACCAGA	GGCAAAAACC	GCTATTTTTT	TCATTTGATA	ATGACACTTT	CGTTTTCTTT	360
CTTGACGATG	CGACCAATTT	CATAGACTGC	TTCATCCAAC	AATTCTTTTA	CACGCTCTAC	420
ATTTTCAGGG	CTGACCGCCA	ACATAAGTCC	CACACCCATA	TTGAAGATTT	CAAACATTTT	480
TTCTGTGTTA	ATCTGACCAT	ATTTTTC AAG	GGCTTTGAAA	ATTGGAAGCA	CTGGAACCTT	540

GCTTTCATCA ATTTTCAGCAG

560

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 860 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTTCAACACT	TTATTTTAT	CTTCTCCCA	TTTCGTATGC	TAGTTCGGAA	ATTGTTGCTA	60
GAACCTCTCC	GACTATTTGG	GATGTTCTCA	TTGCTTTTGT	AGGAGGGATA	GCAGGTATTA	120
TTGGTGCTAG	GAAAAAAGAG	ACCAATAATA	TTGTTCCCTGG	TGTTGCTATT	GCAACCGCCT	180
TGATGCCTCC	TCTTTGTACA	GTAGGTTATG	CTATTGCTTC	TGCTAATCTA	AAATTTATCA	240
TTAGGCTCCT	CTTACCTATT	CCTCATCAAT	TGTAGCTTTA	TTGTCATTGC	GACTTATATA	300
GGTGTTAGGT	TGATGATGGT	TAAGAAACAT	TATTTTAAAG	ATAATGAAGA	AGACTCTAAA	360
ATGCGTAGGA	TTTTGCTTCT	AGTTGCTGTT	TTGCTGATGA	TTCCGAGTTT	CATCTCTGCA	420
ACGACTTTAG	TGAGAGAAAC	GTTGAAAAAA	GAGTCCCTTA	AGAAATTTAT	ATCAGAGCAG	480
TTTCAGGGGC	ATAATATTTT	GAAAAAAACC	TATTCTAAAA	AGACTCATAC	CCTAAAGCTA	540
ACCATTTTCA	GAAATTATTT	GACAGAAGAA	GAAGTCGATA	TGATTTCAAG	TAAGAGAGGT	600
GACTATGGTT	TAAGTGATGT	TTCTGTTCAA	GTTTCACAAT	TGTCTGATTC	AGAACAACCT	660
AGTAAGGAAG	AACTGGTGGA	GTATTTCTTC	CAGTATATCA	AGGATAAGGA	AGCAAAAGAA	720
AAGGAAAAAG	CTAATAAGTT	TTATACAGAG	TCTGAGGAGC	AATAATTTCT	TGAGAATAGC	780
TGGTTTTTCT	CGTGAGTCTT	CTATGTATAT	CAAAGGAAGA	CTGAGGTTTT	AAGTATGAAA	840
CTTTTCTTCT	ATTATAGTAG					860

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 925 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

TCTTGGCCAA	CTGCATGGAG	TTCAGCGGTC	AATTTCAACG	CACCTGAGAA	ACAGACCCCT	60
GCACCCCTGA	AATCTCAGGA	GACATGATGG	TCTGGATGGA	ATCAATAATG	AGAAAGTCTG	120

GCTGGATACG	CTACCACTTC	TGCACGAACA	CTCTGCATAT	TGGTCTCTGC	ATAGAGATAA	180
AACTCACTAT	CAAAATCACC	TAAGCGCTCT	GCACGTAGTT	TAATCTGCTG	GGCAGACTCC	240
TCCCCACTGA	CATAGAGAAC	TGTCCCCACT	TGGGACAAC	GGGTTGAGAC	TTGTAGGAGA	300
AGAGTTGATT	TCCCAATCCC	AGGATCCCCA	CCGATGAGGA	CGAGACTTTC	CTGGTACAAC	360
TCCGCCTCCA	AGCACACGGT	TGAATTCCTC	CATCTCCGTC	TTGGTTCGAT	TGACATTGAT	420
GGAAGTCACC	TCAGCTAGTT	TCATGGGCTT	GGTTTCTCA	CCTGTCAAGG	ACACACGCGC	480
ATTCTTGACC	TCGGCAACCT	CAACCTCTTC	CACAAAAGAA	GACCAAGACC	CACAGTTGGG	540
GCAACGTCCC	AGATATTTAG	GGGAATTATA	CCCACAATTT	TGACATACAA	ATGTCGCTTT	600
TTTCTTTGCG	ATGACAAACC	TCTTTCTATA	TCTCTAACTC	ACACTCAATC	ACTTGGCAAA	660
AATCAATCTT	CTCATTGCG	ACAACTGGC	GCATGAGCAT	TCGATGAGCA	ACAACTACCA	720
CAGTCTGATG	TTCTCGATAC	TTAAACATAC	ATTCTAGAAA	CCGAGACTTC	ATTTCCGTAG	780
CTGTCTCATA	TTGAATAGGA	CTATTAGGAA	GCAACTCCCC	CTTGTTTTCT	AAAAACAGTC	840
TTCTAGCTGT	TTCAAAGTTT	TCTATTCCTG	TTTTATAGAC	CTGCCATTCA	TGTAATAAAG	900
GCTCTACTCT	TAAAGGAAGA	CCCGT				925

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

TTCTNGATCA	AGTCAAGGAC	TGCANGCCAC	GACCGACATA	GCGTTTGGCA	ATGGAAACAA	60
CCAAACGAAG	ATTGGCTTCC	GCAAGACGTT	GTTTGGCTTC	GATATCGCCA	GCTTCAACAG	120
CCAGTGCCAA	CTCTTTCTCC	TCTTCATTGG	TCAAGAGAGG	AACGACCCCT	ATTTCTTTCA	180
AGTACATACG	GACAGGGTCA	TTGACCTTAG	CAGAAGTTGA	CCCAATCAAG	TCCTCATCGC	240
TGAGTTCTGG	TTCTTCTTCA	TTGCTAAGAA	CACGCGCACT	TGGATTTCTT	TCGTTATCTG	300
TGATAGAAAT	GCCTGCATCC	TGAATCCGTT	GCAAGAGATC	TTCAATCCCA	TCAGCGTCCA	360
AGGTAAAAGG	AATAACCAGA	CTTGCAATTGA	TTTCATCATC	TGTTGCTGTC	CCTTTTGTCT	420
TATGATTACG	GATAAATTCT	GCTACCTGTA	CGTCAAATGT	TGTTACTTCT	TTTTGTTTTG	480
TTGCCATTAT	TACTCCATTC	TTCTCTTTTG	GGAAATTAAA	CGTTCCAATT	CTTCTAGGGC	540
TGTATCTGTA	TCTCCTACAT	GGCTAGCTTC	CTGCACCTTC	TTTTTGATTTC	CCATATTGTC	600
CTGATTCAAG	AGAGCCTTGT	TTCGAAGTCA				630

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CTAGGGCCAT	CTTCTCACCT	CCTCCTTGTC	AGTACATTCT	TGCAATAGAA	AAAATAAGAT	60
TGAGTCCCCC	CAACCTTAAA	TTTTTTCACC	ATCTTCTTTT	TCTTTAGCAA	TTTGCTCTTT	120
GATTTTCTTT	TCTTCTTCTT	CTTTGCGGCG	TTTTTCTTCT	TCGATACGGC	GACGCACTGC	180
TTCACGTTTT	CCTTCTGGAT	CTGGGTGAAT	TGTAACGTTT	CCTGATTCTGA	TTTCTTCTAA	240
AGCGCGAAGA	GTTGATTTTT	CAGACTTGAA	ACCTTGAGTT	GCTGGGGCAC	CTGCTTCCAA	300
TTCGTGGGCA	CGTTTTGCTT	CCAAGATTAC	GAGTGAATAT	TTTGAAGGAA	CCTTGTCGAG	360
CAAGGTATCA	ATAGAGGGTT	TTAACATCAT	TTGCTTGATC	CTATTTTCTA	AATTTTATCG	420
GGTAGTTGGA	GATTTTGGTA	ACATCTCCTG	ATAGTGACCA	ATGACACGAT	CCACACAGAA	480
GTGTTCTGCT	TCAATCACAC	ATTTGACACG	TTCAGCAGCT	AGGGGTACCT	GATCGTTGAC	540
AATCGCATAA	TCATACTCAC	GCATGAGGGC	AATTTCTTCC	TTGGCCTTTT	CGATTCTGTTG	600
GGCAATCACT	TCTGCACTAT	CTGTTCCACG	ACCTACCAAG	CGTTCTTGCA	ATTCATCCAA	660
ATCTGGTGGT	GTCAGGAAGA	TAAAGACAGC	ATCTGGAACC	TTTTTCTTGA	CCTGAAGAGC	720
ACCCTGAACT	TCAATTTCAA	GGAAAACATC	GATTCCCTTG	TCCAAGGTTT	CATTGACATA	780
GGTCAGAGGA	GTTCCATAGT	AGTTGCCGAC	ATATTCTGCG	TATTCCAACA	TCTGTCCTTG	840
ACGAATCAG						849

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 581 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GCCAAACAAC	GCATCCATAA	TGGTTAAATC	TTGATAAGGC	AGAGCTACAT	TCAAAACAGC	60
TTGCTGGTTT	GTAGGCTTTC	AATCAGAGCA	ATCACTTCTT	CAACCTTGTC	AGCATCAAGA	120
GCAGCTGTCT	CAATCTTTGT	ACTTGTTTTG	CCTTCCAGTT	TAGCTTTCAA	GTCATCGCAT	180
TTTGACTTGG	TACGGCTAGC	AATCATAATC	TCTGTAAATG	TTTCGCTATC	TTGACAAATC	240
TTTGAAATAG	CAACTTGGGC	AACGCCCCCA	CAACCAATAA	CTAGTAAACG	ACTCATTTTTT	300
TTCCCTCCTC	TTCTTCTAAA	ATGTCCTCAA	CATACTTGGG	CAACATAAAG	GCTCCCACGT	360
GTAAGTTTGC	AGTGTAGTAT	TCTGTGAAAA	GCTGGCGTTT	TTTCCAGCCT	TCCTTGTCAT	420
AATCTTTGAC	AGGGTGGTAT	TTTTTCGATG	CAAATCCAAA	CAACCAATAG	CCAGCTGGGC	480
TAGTTGGAAT	ATGGGCCTGA	TAAACCCGAC	TGATTGGAAA	GGCTTGATTG	ACCTTGCGGT	540

GCATGCTTCG GCAGGCCGAC TCATCCTCGT CAAAGAAAGG A

581

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TTCTGAAAT	CCATACTTCT	ACCAAGGAGA	TACGCTAGCG	GTCTCGGAAG	TTCTCATACT	60
TCTATCGCTA	TATCTGGCCA	TCGCCTTTCT	ATCCAAGGAT	TGACAACAAG	AGATAAGGCA	120
GAGAAAAAAT	TCTTGCTGGA	TCAGCTGGTT	GCCTGCGATG	GTGGTACAGG	TGTCATGCAC	180
GAAAGCTTCC	ATGTAGATGA	TCCGACCCTC	TACTCTCGTG	AATGGTTCTC	CTGGGCTAAC	240
ATGATGTTCT	GTGAGTTGGT	CTTGGATTAC	TTGGATATTC	GCTAAGGGGC	TGCCTTTAGC	300
TCAACCGATT	CTTATCAGAA	TCACAAGTTT	ACATTTAAAA	CGTTAAAATT	TAAATTTAGA	360
ATGAGGTTTT	ACTTCATGGA	AAATGTTGTT	GTACATATTA	TCTCACATAG	CCACTGGGAT	420
CGTGAGTGGT	ACTTGCCTTT	TGAAAGCCAT	CGTATGCAAT	TGGTGGAATT	GTTTGACAAT	480
CTCTTTGATC	TCTTTGAAAA	TGACCCTGAG	TTCAAGAGTT	TCCACTTGGA	TGGACAAACT	540
ATTGTCCTTG	ACGACTAACT	TACAAATTCG	CCCTGAAAAAT	CGCGACAAGG	TCCAACGCTA	600
CATTGACGAG	GGCAAGCTTA	AAATTGGTCC	CTTTTACATC	TTGCAGGATG	ATTATTTGAT	660
CTCCAGTGAA	GCCAATGTCC	GCAATACCTT	GATTGGTCAA	CAAGAAGCTG	CCAAATGGGG	720
TAAATCAACC	CAGATTGGCT	ACTTTCCAGA	TACCTTTGGA	AATATGGGAC	AAGCGCCTCA	780
AATCTTCAA	AAATCAGGCA	TTCACGTGGC	GGCCTTTGGT	CGTGGTGTGA	AGCCGATTGG	840
ATTTGACAAC	CAAGTCCTTG	AAGATGAGCA	GTTTACGTCT	CAGTTTTCAG	AAATGTACTG	900
GCAGGGTGTG	GATGGTAGTC	GTGTTTTAGG	TATTCTCTTT	GCCAACTGGT	ACAGTAACGG	960
GAATGAAATT	CCAGTTGACA	AAGATGAGGC	CTTGACCTTC	TGGAAACAAA	AATTGTCAGA	1020
TGTGCGTTGC	CTACGCTTCG	ACCAACCAAT	GGTTGATGAT	GAAACGGCTG	TGAACACCAG	1080
CCTGTCCCAA	AAAAAATCTG	AGCGAAGCCA	TTCCGTGTGG	CAAATGAACT	CTTCCCGGAT	1140
GTAATCTTTG	TTCATAGTTC	TTTGTATGAA	TATGTTCAAG			1180

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CTCAAAAAGT	CTGAAATTGG	ATCATTTGGA	ACCATCTGAG	CAGTAAGTTT	AACACCTTTT	60
TCTGCCAGTT	TGTGGAAGTC	TTCCACATCC	TTGTCTACTA	CGTTGATAGA	ACGTGTAATA	120
GAACGAGTTT	CTGGTGTGTTG	AGACATATTC	CCAACATTAA	GGGTTTCAAG	TGGTACACCT	180
GCTTCTACCA	AACCAAGGGA	AGCGGTCTGG	TTTACGAGCC	ACGATAAAGA	GACGTTGGCT	240
ATCGTATTTG	CCAGCAAGAA	TATTGGCTGC	AGCTTTCTCA	ACTGGCAAAA	TACTCAATTT	300
CACACCTGGT	GGTGTGCGAA	GTTTCAAACC	ACTCTTTTCA	ATATCGTTGT	TGACAACTTC	360
GTCGTCTACA	ACCATAATGC	GTGAAACATT	TAGTTTTTCCA	GCCCAAAGAT	TGGCTACTTG	420
TCCGTGGATC	AAACGTCCAT	CAATACGGCA	TCCTACAATT	GTCATAAGTT	TTCCCCCTTT	480
ATATGTTTTA	GTGTAGGTTT	ACGAGTTAAA	TGAATCTCTT	CTTTATATTG	ACCTTCTGTT	540
TCAAAGATAA	TGATGCGGTT	GGCACCTTCC	TTGAGATAG			579

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 736 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CGCATANCCCT	AAAAGTTTTTC	TTTGACATCT	TCTGGAATAT	CTGTATCATT	AGCTTCCTGA	60
ACATCTCTAC	CATAAATCCC	AAAGGCTGGA	ATCCCTTTTT	GAGCATGTGA	AGCTAGTACA	120
GCTGCAAGAT	AGACAGCTCC	TGGGCGTTCT	GTCCCATTAA	ATCCCCAAAT	AGCATGAGGA	180
ATATCTGGAG	ACATATCCAT	AGTTTCACTA	CCATAACACC	AGCATGGTGT	AAGTGAATT	240
GTTGCGCAAA	CATTTGATTT	TTTAAACAAC	TCATGGGAAG	CTGCAGCCTC	TGGAACACGA	300
CCAATGGTAG	ATGGAGAAAT	CACACATTCC	ACAGGTTCCC	CATCTGGATA	TTTCAATGTG	360
CTTGAAATCA	AATCTGCCAC	ACTTTTAGCC	ATGTTCAATTG	TTTGTACTTC	AAGTGATTCTG	420
CGTACACCTT	GACGACGACC	ATCAATAGTC	GGACGAATCC	CAATACGTGG	ATGTTGAATC	480
ATACTATTTT	CCTCTTATTT	TTCTGTTTCT	TTCATACTAC	CATCGCCATT	ATATTTACGG	540
TAGCCTGGGT	GACGACCTGT	AACCTTATAA	TTTTCTCGCA	TTGAGAATAG	ACGTTCTAAA	600
GTCGGACGAG	CAATTTCTTG	CTCCTCAATG	CCCTTTGTAG	AAAGTAACAT	TCTTCCGTGG	660
AAGTTGTCT	TTGCGACTAA	TTCTAAAGTT	TCCATACGGT	AGTATGCTGT	AATTACATCG	720
CTTCCGACAG	TCAGAG					736

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTCATTGTAT	TTAGGAGAAA	TGATGGTATC	TTCCAAATCA	AAATCAACTT	CACTCCATAG	60
TCTCAACGGA	TTGATTTTCC	CATCTTGATA	GGTCACATCC	TTGTCAAGGA	TAAACTGAGT	120
CAACGCCTCA	TGCTGACCTT	GACACCTGAT	GTCATCTACC	AAGAGCCAGA	CATCCTCTAC	180
CAACATGAGG	ATTTTCTCT	TGTGAAGATA	AGGCAAATCA	GGTTCTGCTG	ACCAATAAGC	240
CCCTTCAATA	TAATGCATTC	CCTCCCTTTC	TTTATGGTGA	CAAAACAGGG	AGTGAGGATA	300
GTATTCATAT	TCCCAGGATC	CCGTGATTCT	TTCCGGAGCT	TTCCCATCTA	CAATGCAGGT	360
CGAATGACTC	CAAGCACTCT	TTAAGAGATA	ACGTTTCATAT	ATCTCCCGAT	AAGAATAACG	420
CCCAGCATCT	ATGAAAATAG	GTTGGCCTTG	ATACTGTAAG	CAAAACTAT	TCTCGTCACT	480
ATGGCTATGG	GCACTTCCTA	GCGGACCATT	TTTGAAAAAT	AGATAACGAT	GTTTCATCCTT	540
AATGCAGACA	TGTCCAGAGT	CTTCAAAGAT	CATGGACTTA	GGCTGCCAAG		590

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1199 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CTAGTGTAGC	TTCCTTAATC	TTATCTGATA	AGATAGCTGT	CATATCAGAC	TCAATCATTT	60
CCTGGAGCAA	TCACATTGAC	TCGTATATTC	CGACTAGCGA	CCTCGCGTGC	CACAGACTTG	120
GTAAAGCCAA	TCAAGCCAGC	CTTAGAAGCA	GCATAGTTAG	CTTGACCAAT	ATTCCCCATC	180
AAACCAACAA	CACTAGACAT	ATTAATGATA	GCACCTTCTC	TGGCTTTCAA	TCATCGGTTT	240
CCAAAGACTG	ATTGTGTCAT	ATTAAAGGCA	CCAGTCAGAT	TGACCTTGAG	CACTTTTTCA	300
AAATCTGCTT	CTGTCATCTT	GAGCATAAGA	GSTATCTTGGG	TAATCCCTGC	ATTGTTGACC	360
AAAACATCTA	CTGAACCCAG	TTCTGCAATA	GCTTGATCAA	TCATACGCTT	AGCGTCTGCA	420
AAATCTGATA	CATCTCCTGA	AATGGGAACC	ACCTTGATAC	CATAGTTTGA	AAACTCAGCG	480
AGCAATTCTT	CTGAGATTGC	CCCACGACTG	TTTAAGACAA	TGTTGGCTCC	TGCTTGAGCA	540
AACTTGTGGG	CGATGGCAAG	ACCAATTCCA	CGACTCGAAC	CTGTAATAAA	GATATTTTTA	600
TGTTCTAGTT	TCATTTTTTT	CCTTTCAAAA	CTTCTACTTA	TTTGTAGTCTA	TTTTTCTAAA	660
AGTGCTACTA	AACTCGCTTG	ATCTTCCACA	TGAGCTAAGT	GAGCAGTTTG	ATCAATTTTTT	720
TTAACAAAAC	CTGACAAGAC	TTTCCCCGGT	CCAATCTCGA	ATAAAGTTGC	TTATGCCTGC	780

TTCTTGCATG	ACCCCAATAC	TTTCATAGAA	ACGAACGGGT	TCCTTGACCT	GACGCGTCAA	840
GAGCTGAGCA	ATGTCTCTT	TTTGCATCAC	AGCAGCTTCT	GTATTGCCGA	CTAGGGGACA	900
AGTAAAATCT	GAAAACTTA	CCTGAGCTAG	AGTTTCAGCT	AGTTTCTGGC	TAGCAGGCTC	960
AAGGAGAGCG	GTGTGAAAGG	GACCTGACAC	CTTAAGAGGA	ATCAAGCGTT	TGGCACCTGC	1020
TTCTTGCAAA	AGTTCAACCG	CTCGATCAAC	TGCAACCACT	TCTCCAGCAA	TGACGATTG	1080
TGCAGGTGTG	TTATAGTTGG	CTGGAGTAAC	CACTCCAAGT	TCCAGAAGCT	TTTTGACAGG	1140
CTTCTTCAAT	GACCTCTACT	GGCGTATTGA	GAAGTGCTAC	CATCTTGCCA	AGTTCAGCA	1199

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CTACTATTTT	CTTTGCCATA	GCCTTCTCCT	TTACACACTA	CGCATATCGT	GGTAAGAAAC	60
ACTGCGTCCC	ATCTCACCTG	CATTCTCTTT	TTGAACAAAG	GTATTAGCGT	TTATATAGGC	120
AATAGCAGAA	GCCTTCAACA	CATCAAAATC	AAGCCCTGCT	GCATTAAAGA	TGGTTTCTGT	180
ATCCCTGTTT	TCAACAGTGA	CCAACAACCC	GATCCTGGGC	ATCGATTCCA	TCTGTTACCG	240
CATTGATAGT	GTAGGACACC	AAACGAACAG	ATTGGTTAAA	GAACCTATCG	ATAGCGTTAA	300
AGATTGCTTC	AACGGAACCC	TGTCCCTGTC	GCATTAAATT	CGACTTTCTC	ACCATCCATA	360
TTGGCTAGGC	TAACGAGCGC	TTCAATGTCA	TTATCTGCAT	GAGTTTGAAG	TTGTAAATCA	420
TCAAAGTGGA	AGCCTTCTGG	ATTTTCAACC	ATGGTTCCAG	CTACCAAAGC	TGCAGTATCT	480
GCATCTGTGA	TTTCTTACTT	CTTATCGGCC	AGTGCCTTGA	ACTTAGCAAA	GAATGGTTTG	540
ATATCCTCTT	CTGTAAAATC	TAAGGCCAAT	TCTCTCAGTT	TCTCAACAAA	AGCATGGCGA	600
CCAGATAATT	TTCCAAGCGG	AATCTTAACA	CCAACCAATT	CAGGTGTGAT	GATCTCATAA	660
GTGAGAGGAT	TTTTAAGGAC	TCCATCTTGG	TGAATACCAG	ATTCGTGGGA	GAAGGTATTG	720
CCACCAACGA	CGGCTTTGTT	TTTAGGAACT	GGAATACCAG	AGAAGCGAGA	AACCATTTCT	780
GACGTATTGA	TGGTCTCATT	TAGGACAATA	CTGGTTTCTA	CTTGGTAGTA	ATCTTGGCGA	840
ATATTGAGAG	CCACTGCAAT	TTCTTCCAAA	GCAGCATTTT	CAGCTCGCTC	CCTAATACCA	900
TGGATAGTCT	CTTCAAAAAG	TCCTGCACCA	TTCTTGACAG	CAGCAAGGCT	ATTTGCCACT	960
GCCATCCGAA	GTTTCATCATG	ACAGGGAGGC	GAATAGATGA	TCTGACGATC	CGTCTGGACA	1020
TTCTCAATCA	GGTATTGGAA	GATGGCACCA	CATTCTCTCTG	GTGTGGTAAA	TCCTATATTT	1080
TCTGAAAATT	TCTTCAGTAA	AGAATATTTA	GCTAATTGAA	AGTTCATGAA	AATTATTAAA	1140
ATATTTTCAAT	TTTTAGAGGT	TAAGTTCCAA	CTTTTTTCTA	TCAATTCCAG	TACTTNTTCA	1200
TCTGATAAAG	TATCATCAAG	GGACACACTA	ATCCAGTAGC	GCTTGCTCAT	ATGGAAGGCT	1260
GGATAAATCC	CCTTTTGTGA	AAGCAAATTA	GCTACTTGGT	CATGCTTGAG	GTTGACTGCT	1320
TCCACTTGTC	CTTCTCTGCC	CTTTTCCAGC	TTATTCCAAG	AGATTTTCAN	CAAGACGGCA	1380
TACCACTTTT	GATTGCCTTC	ATGGCGCAAT	ACAG			1414

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CTCCCCATTT TGGAAAATTT CTGTCAAGAA ACGGCGAACC AGCTTTTTTAT TTTCTGCTTT	60
CTTGTCCTAAA TCCTTGATTT CAAAATCTCC AAAAATTTGA TCTAGTTGGT CATTTTCAGG	120
TGTTTCGATAG TAGTCAATGA CATCCCAATG CTCAACAATA CGACCATTCT CATCCGCACG	180
GAAAGTATCC GTCGTCACCC ATTGAGCTTC TCCACCATTG AGATATTGAT GGAACATGAA	240
CAAAGACCAG ATTGCCATCC TCAATGGTGC GGACAATCTT AATCTGACGC TCTGGATGAC	300
GCTCAAAGAA ATCTGCAAAG AAGGCTGCAA ATCCTTCTTT CCCGTCAGGA ACACCTGTCTG	360
AATGTTGGAT ATAGGTATCC CCTACAGACT GGGCTTGAGC CTCAGCAACT CGTCCGTCTT	420
GAATGGCATG GATGTATAGG TTGTGAGCAT TTTTCACTTG TTGTGACATA TTCTAAACCT	480
CATTTCCCTT CTCTTTCAGA TTCGCCAAAA TTCTTTCTTG AAAACCTTCA AATTGGTGAA	540
TTTCTTCTC TGAAAATCCT TTGTAAAAGA TAGTATCCAA TTTCTGACTG ACACGATGCC	600
CCACTTCTTT CTGGGACTTG CCTAACTCCG TTAAACTAA ATACTTCTTA CGCTTGTCTT	660
TTCCACACGG ACTAACAATT ACAAGCTTTT GTTCCTCTAG CTTTTTTATC ATAGTCGTCA	720
GCGTATTATT CGCAAGCCCA GTCGCAAGCG	750

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 953 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GTATCGTTCA ATTCCAAAGA TACGGAGGAA GCTGCGTTTC GCGAGAAAAC TCTTGTTAGA	60
CCAGATAGGG ATTAGCCAAA ATCCTTCTAT GNGCTTATAT CCAAATGGAG ATGCAAACTT	120
CTGCCCAACT CTTGACCAAT AAGATCTTTC TTAAAAATCC ACTCAAGGCT CTGGTAGAGG	180
AAAAATATGG GATTGAGTAT GAAGAATTGA CCAATCCTTG GCACGCTGCC ATTTCTAGCT	240
TCGTTGCCTT TTTCCTTAGA AGTTTGCCCTC CAATGCTGTC AGTGACCATA TTCCCAAGTG	300

AATATCGCAT	CCCTGCTACT	GTCCTTATTG	TCGGTGTGGC	CCTTCTTCTC	ACTGGTTACA	360
CTAGTGCCAG	ACTTGGAAG	GATCCGACTA	GAACAGCTAT	GATTCGGAAC	CTTGCTATTG	420
GTCTCTTGAC	CATGGGAGTT	ACCTTCCTGC	TCGAACAAC	TTTCAGCATT	TAGAATACAA	480
GAAATACCTC	GATTTTGAAG	TCGAGGTATC	TTTTTTACAT	TTGCACAATC	TTGCGATAAC	540
TTCTTGAAGT	AATCATGAAA	ATCAGCACAT	AGGCGATGAG	GAAGATAGCG	CAGATAGACA	600
AGGTCACAAT	CAACATCATA	GTCGTATCCA	GTACACCAAT	CACTTTTAAA	ATCAGGCTAA	660
GCATATGGTA	GGCAAAGGCG	AGATGTATGA	AGGCAAAGAG	CAAAGGAAGG	AAGAAAACAG	720
TTAAACCTG	TTTGTTGATG	GTTTGCTTGA	TTTGCTTTTG	GTCCAAACCG	ACTTTCTGCA	780
AGATAATAAA	GCGTTCACGG	TCTTCGTAGC	CTTCAGAAAT	TTGTTTGTAG	TAGATGACCA	840
GAACAGTTCC	GACCATAAAG	ATAATGGATA	GGAAAATACC	GATAAAGAAG	ACACCGCCAA	900
AGAGGACACT	CATTTGAGCA	CTAGCATCTG	CTAGATTGCT	ACCATAAACA	TAG	953

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CTGATTGAAC	TTCTATTTAC	TAATATTCAA	AAATCCTCCG	TTTCAAAGAG	CAGGGAAC	60
TTTGTGACAG	AGGATTTTTT	CTATAGGGCT	TTAGCAGCTG	CAATTGCGGC	TTCGAAGTTT	120
GGCTCAGAA	TGATATTATC	CACGTATTCA	ACGTAGCGAA	TCGTATTGTC	AGTATCGAGG	180
ACAAAGACTG	CGCGTGCTAA	TAGGTGCCAT	TCGTTGATCA	AGAGGGCATA	ATCGCGCCCCG	240
AAAGAATGGT	CAAAGTAGTC	TGAAAGCATA	ATGGCATTGT	CAAGGCCTTC	AGCACC GCAC	300
CAACGTTTTT	GAGCAAAGG	TAGGTCCATT	GAAACAGTCA	ATACGACCGT	GTTGTCCAGT	360
CCAGCCAATT	CTTCATTAAA	ACGACGTGTT	TGAGTTGAGC	AGATGCCTGT	ATCGATAGAA	420
GGAACGACAC	TCAAGACTTT	TTTCTTGCCA	TCAAAATCAG	CCAGAGATTT	TTTAGAAAGA	480
TCTGTTGTAG	TAAGAGAAAA	ATCAAGCGCC	TTGTCGCCGA	CTTGTAGTTG	TTTACCTGTA	540
AAGCTCACAG	GATTTCCGAG	AAAAGTTACC	ATAGGATACT	CCAATCTTTT	TTCTTCCATT	600
GTATCTGAAA	CAGTCAGAA	TTTCCAATGA	TTTGACCGGA	AATGTGGGCA	TAGAAAAAAC	660
GCCAG						665

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1039 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CTAAGTATAA	AAAACCTTGCC	GAAAGTATCT	CTGAAGTTAA	TTTGAATGTC	TTTTTTCAAA	60
ATGCTTTAGA	TTTTGTTGAA	ATCTTTAATC	AAGAGCCTTG	TCTGATAAAT	TTTTTTGAGT	120
TTATGAATTC	TATGTTACAA	GGCGATATTC	CAAAGTTAAC	AATAAACCAA	GAATAATAAG	180
AGGGGAACAG	TATGAAAGAT	ACGATTTCTA	ATAAGGATTT	GATTTCCATG	GGCTATAGAC	240
CATCAACAGC	AAATGCTATT	ATCCATCAGG	TGAGAGAATT	ACTTGTATCA	CGAGGCTATA	300
CATTTTATAA	TCGCAAACGT	TTGATGGTTG	TTCCAAAAAG	TGTTGTGAAA	GAGTTGTTGG	360
GAATGGAATT	GTGAAATGGC	TTATATCGAG	TATAAACAGC	GTGGGAAGAA	AAGGCTTTGG	420
TCGTTTTCTA	TACGTGAGAG	GAGCAAGAGC	CTACTCCATA	AAAGCGGATT	TAAAACAAAA	480
CGAGAAGCTA	AAATAGAAGC	GGAGAAAGTT	CTTCATAAGT	TAAATACTGG	GAGTGTCTTA	540
AGCTCTAGTA	TGACTTTATC	GGAGCTTTAT	AATGAATGGC	TGGATTTAAA	AATTTTACCT	600
AGCAATAGAA	GTGTAGTTAC	TAAAAAATAA	TATCTTATGA	GAAAGAAGGT	CATCGAAAGG	660
TTATTTGGAA	ATAAGCCTGT	ATCACAAATT	AAGCCTAGCG	AGTATCAAAA	AATTATGAAT	720
GAGTATGGAG	AGACTGTATC	GAGAAATTTT	TTAGGAAGAT	TGAATTCTAG	TATCCAGGCA	780
AGTATACAGA	TGGCTATTGC	TGATAAGGTG	ATAATAGAGG	ATTTTACTGC	TTATGTTGAG	840
TTGTTCTCTT	CTAAGAGTGG	ACACAAAGGT	TGAGGAAAAG	TATCTACATA	CTGAGTCAGA	900
TTATCAAAAA	GTTTGTAGTAT	ATTTGAAAAA	TAAGTTTGAT	TATCAGAAAT	CTATTGTACC	960
GTATGTAATT	TATTTCTTTT	TTAAACTGG	CATGCGTTTC	TCCGAATTGA	TTGCTCTAAC	1020
TTGGGATGAA	GTTGACGAG					1039

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CTGAGAAGTC	AGGAAGGCGA	TGTGGAGAGA	TTGAGGAATT	GGATACTTAA	CTCCATAGTA	60
ATCTTCGTAA	AACTCGATAG	AGCGAACAGC	GATATCCAGT	GAGAAATCAA	GATTTGAAAG	120
TGGATGTGCT	TTGGTTGAGT	AGACACCCTA	CCAGGGTACC	ATTTTGTAGT	TTAGCGGTCA	180
CCCCTTGCAA	ATCACCAGCA	ACAAAGGCCA	ACAAGTAAGA	AGACATGCGA	GGTGTGTGCT	240
CAAACCTCCA	GATACCTGTT	TCCTTACGGT	TTTCAACATC	GATTTCTGGC	ATGTTTGACA	300
AGGCCAATTC	ACCTTCTGCT	TGGTCAAAGC	GAAGAGAGAG	GTCAAAAGTT	GCTTTGGCTT	360
CAGGCTCATC	CACACATGGG	AAAGCTTCGC	GCGCAAAATG	GCTCTCGAAC	TGAGTAGACA	420
AGACCTCCTT	CTTGACTCCA	TCAACTGTAT	AATAAGAAGG	GTAAATCCCT	GTCATGTTGT	480

CTGTAATTTT ACCAGAAAAG GCAAGAACCA ATTCAACTTG ACCAGCCTCA GCCAATTCGA	540
TATGAAGGGC TTCATTGTCA TGGTCAACTG TAAATGGACG AGCTTGACCT GCAACTTCTA	600
CAGAGGTGAT TTCCAAGTCT TTTTGGTGA GGGAGATGCG GTCACCTCTGT GCTTGACCAG	660
TGATGGTCAC TTTCCCAGAA AAAGTCTTGG TCTCACGACT CAAATCTAAA AATAAATCAT	720
AATGTTTCAGG AACAAATTGC TTAATAAAAT GTTCAACTGC TTGCATAGTT TTCTCCTATT	780
CTAAGTTTAA GAG	793

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CGGATGATTT GCTTTTCATC TATGATAAAG TCTTTGTTGA GCGTCGGAAT CTCTACTGAC	60
TGGAAATTTT CCGTAGATAA TCCAAATGCC CTTTAAAGAA AACCTCATCT GTCAACACCG	120
AAATCATCAC TGCTCCGTTT TCTTCATAAG TCTGGGCCTG TTGCACAATA TCCACATCGA	180
GATTGATATC TCCCCAAAAC TAGGGCTAGC TTTCTTGACT TCAGCGATTA CCTGCAAGCG	240
GTCCTGATGA TTCTTCAAAA ATTCTGCCAA GCGATAGGTC TGGCGCAGAG GCTGGATTTG	300
CTCCAGCTTC ATCTGCTCCA CCTCACGCGC CTTCTGCTCT AAGATTTCGTG CTAAAAATTC	360
CTGACTCATT TTTGGTACTC CTGTAACAGT CTGAGTTTTT CAAGGGCCTT GCCTCTAGCA	420
ATCACTTGAC GGGCCAAGGC AACTCCTTCC TTGATGCTAT CAATCTTACC ATTAGCATAG	480
AAACCAAGAC CAGCATTCAA GACTGTCGTT TCCAAGAATG GACTTGCTTC GTTTTTCAGA	540
ACGCTAAGCA AAATTTCTGC ATTTTCCTGA GCATTCCCAC CACGAATATC TTCCATAGCA	600
TAGCCTTCCA TTCCCAAATC CTCTGGAGTA AAGCTTGACA AG	642

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 733 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CTCTTGCAGG TTATTAAGGA GAAAACGGAG GTAATAGAAG TATGATTTAT ACAGTCACAC	60
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TCAATCCATC	CATTGACTAT	ATCGTTCGTT	TGGACCAAGT	CAAAGTTGGT	AGTGTAATC	120
GTATGGACAG	TGATGATAAG	TTTGCTGGTG	GGAAAGGAAT	CAATGTCAGC	CGTGTCTTGA	180
AACGTTTGAA	TATATCAAAT	ACAGCGACGG	GATTTATCGG	TGGCTTTACT	GGTAAATTTA	240
NCNCAGATAC	TTTAGCAGAG	GAAGAAATCG	AGACNCGTTT	TGTCCAGGTG	GCAGAAGATA	300
CTCGTATCAA	TGTTAAAATC	NAAGCAGACC	AAGAAACAGA	AATCAACGGA	ACGGGTCCAA	360
CTGTTGAACC	GGTTAAGCTA	GAAGAATTGA	AAGCTATTTT	ATCTAGTCTG	ACAGCAGAAG	420
ATACAGTTGT	CTTTGCAGGT	TCAAGTGCTA	AAAATCTAGG	CAATGTTATC	TATAAGGGAT	480
TTAATCTCCT	TGACGCGCCA	GACTGGTGCG	CAAGTGGTCT	GTGACTTTGA	AGGACAGACC	540
TTAATTGATA	GTTTGGATTA	CCACCCTCTT	CTTGTA AAC	CAAATAATCA	TGAACTTGGA	600
GCGATTTTGT	GGGTAAACT	CGAAAGTTTA	GATGAAATTG	AGAAATACGC	TCGTGAGTTA	660
CTGGCTAAGG	GTGCTCAAAA	TGTTATTATC	TCTATGGCTG	GTGATGGTGC	CCTTCTTGTC	720
ACATCTGAGG	GAG					733

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CTAAGGGAAG	TAGGAAAAGT	ATGTATCCAG	ATGATAGTTT	GACATTGCAA	CACGGACTTG	60
TACCAGATCA	ACATGATGCA	GGTTTACTTT	GATCAAGGGA	TTTACAATAA	GAAGGCGGTC	120
TTTGAGGTGT	ATTTCGCCA	ACAGCCTTTT	AAGAACGGCT	ATGCGGTTTT	TGCAGGTTTG	180
GAAAGAATTG	TGAACTATCT	TGAAGACTTG	CGTTTTTCAG	ATAGTGATAT	AGCCTATTTG	240
GAGTCGCTTG	GTTATCATGG	GGCGTTCTTG	GATTACCTTC	GCAATTTCAA	GTTGGAGTTG	300
ACCGTTCGTT	CTGCCCAAGA	AGGGGATTTG	GTTTTTGCTA	ATGAACCGAT	TGTGCAGGTG	360
GAAGGACCTC	TAGCCCAATG	TCAGTTGGTC	GAAACGGCTC	TTTTGAACAT	CGTCAACTAC	420
CAGACCTTGG	TGGCGACGAA	GGCAGCCCCC	TATCCGTTTG	GTTATCGAAA	ATGAACCCTT	480
GATGGAGTTT	GGGACACGTC	GGGCTCAAGA	AATGGATGCG	GCCATCTGGG	AACACG	536

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CTGCCCCGTG	AAGGCTGGAC	GATTGCCTTT	CTTAGTATCC	GCAAAGAGGT	AAACTGAGAA	60
TAGAGAGGAT	TTCTCCTTCA	ATATCTTTGA	CAGACAGGTT	CATCTTGCCT	TCTACGTCTG	120
AAAAAATCCG	CATATTGACC	AGTTTTCTCA	CAGCATAGTC	CAAATCTTCC	TCTTGGTCCT	180
CTGGTCCAAC	ACCAACCAGC	AATAAAAGTC	CCTGATTGAT	TTTTCCCTGA	ATCTGGCCTT	240
CTATACTCAC	TTGGGCTTTT	TTAACCCGTT	GGATAATGAT	TTTCATAATA	GCCTTTCTAG	300
TAAGAGCTAG	GACAACTAGC	CGTTGGTCCG	TTTGACAGAG	TAAACTTCTG	GCACACTCTT	360
AATTTTATCG	ACAACCGTGG	TCAGTGTAGA	GAGGTTGGCA	ATACCGAAGG	ACACATGGAT	420
ATTAGCAAAC	TTCATATCCT	TGGTTGGTTG	GGCATTGACC	GTTGAAATAT	TCTTGGTTGT	480
ATTTGAAAAG	ACTTGCAGTA	CATCGTTCAA	CAGTCCTGTA	CGGTTGAGAC	CGTAGATATC	540
GATATGGGCC	ATATACTCCT	TATTTGAG				568

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CTTTATATTG	TACCAAGTAT	CATTTCTAGT	GCTGCTATGG	GCTTGATTTT	TCTTCAAATC	60
TATAATCCAA	ACTATGGTGT	TGTTAACCAA	ATTATTCATC	TATTTAATCC	ATCGTTTAAA	120
GATTCAGTAC	TGTTGACTCC	CAGGATTAAA	AATAGTAGCT	ATGACTGGCG	CTTATATCTT	180
CTTTGCAGGA	GCATCAACCA	TTATGATTTT	TTGGGCAAAT	TTTTGCTATT	CCAGAAGAAG	240
TTCAAGAAGC	TGCTATTTTA	GACAATATTA	CTGGTTGGAG	GAAAGAGTGG	TATATTACGA	300
TTCCGATGAT	TAAGGGGACA	ATTAAAACTG	TTTCAATTAT	GGCAGCAACT	TCAGGATTTT	360
TGCTCTATAA	CGAAGTATTC	TTTTTGACAA	ATGGTGCTGC	AGGAACAAAA	AGTATCAGTT	420
TTGTTATTTC	AGAATTAGCA	GTGGCTAGCT	CACGAACTCA	GTATGCTCGT	GCAAATACAA	480
TTGGAGTTAT	ACAAATCTTA	GGTGGAATGT	TGATTATCGT	TTGTATTAAT	ATTTTATTCA	540
GAGAAAGAAA	AAGACTGAAA	GGTGGGAAAT	GATTATGAAT	ACACATATAA	ATGGTATTAG	600
TAAAAAAGGC	AAAGTTCTTA	TATATGGTTA	TATGCTCCTT	ACCATTTTAA	TTTCTATTTT	660
CCCTATTGCG	TGGATTTTTT	TATCATCATT	AAAAGCAGAT	CCTATGAAAA	ATCCAGGTAT	720
TAGTTTACCG	ACTGACTTTA	CTCTTGAAGG	TTATATAAAT	GTTTTTACAA	AACTTCATGT	780
TTTTACTTAC	TTTTGGAATA					800

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CTCAGTATTA TCCCTACCAA AATGAACGTC AGTTAGTGAC TCAGGTGGTT TGGGAACAAT	60
GGGCTTTGGA ATTCCAGCAG CAATCGGTGC TAAAATTGCT AAGCCAGATA AGGAAGTAGT	120
CTTGTTTGTT GGGGATGGTG GTTTCCTAAAT GACCAACCAG GAGTTGGCTA TTTTGAATAT	180
TTACAAGGTG CCAATCAAGG TGGTTATGCT GAACAATCAT TCACTTGGA TGGTTCGCCA	240
GTGGCAGGAA TCCTTCTATG AAGGCAGAAC ATCAGAGTCG GTCTTTGATA CCCTTCCTGA	300
TTTCCAATTG ATGGCGCAGG CTTATGGTAT TAAAACTAT AAGTTTGACA ATCCTGAGAC	360
CTTGGCTCAA GACCTTGAAG CTACTACTGA GGATGTTTCT ATGCTAATTG AGGTAGATAT	420
TTCTCGTAAG GAACAGGTGT TACCAATGGT ACCGGCTGGT AAGAGTAATC ATGAGATGTT	480
GGGGGTGAAG TTCCATGCGT AGAATGTTAA CAGCAAACT ACAAATCGT TCAGGAGTAC	540
TCAATCGCTT TACAGGTGTC CTATCTCGTC GTCAGGTAA TATTGAAAGC ATCTCTGTTG	600
GAGCAACAGA AGATCCGAAT GTATCGCGTA TCACTATTAT CATTGATGTT GCTTCTCATG	660
ATGAAGTGGA GCAAATCATC AAACAG	686

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TTTTCCCAGC TATTTTACTG AGTATAAAAG CCTTATTTAA CTTACTCTAT GTACTCGGTT	60
TTCTAGGAGG AATGTTGGGA GTTGGGATTG CTTTGGGGTA CGGAGTGGCC TTATTTGACA	120
AGGTTCGGGT GCCTCAAACA GAAGAATTGG TGAATCAGGT CAAGGACATC TCTTCTATTT	180
CACAGATTAC CTATTCGGAC GGGACGGTGA TTGCTTCCAT AGAGAGTGAT TTGTTGCCGA	240
CTTCTATCTC ATCTGAGCAA ATTTCGGAAA ATCTGAAGAA GGCTATCATT GCGACAGAAG	300
ATGAACACTT TAAAGAACAT AAGGGTGTAC TACCCAAGGC GGTGATTCGT GCGACCTTGG	360
GGAAATTTGT AGGTTTGGGT TCCTCTAGTG GGGGTTCAAC CTTGACCCAG CAACTAATTA	420
AACAGCAGGT GGTTGGGGAT GCGCCGACCT TGGCTCGTAA GGCGGCAGAA ATTGTGGATG	480
CTCTTGCCTT GGAACGCGCC ATGAATAAAG ATGAGATTTT AACGACCTAT CTCAATGTGG	540
CTCCCTTTGG ATCGAAATAA TAAGGGACAG AATATTGCAG GGGCTCGGCA AGCAGCTGAG	600

GGAATTTTCG GTGTAGATGC CAGTCAGTTG ACTGTTTCCTC AAGCAGCATT TTTAGCAGGA	660
CTTCCACAGA GTCCCATAC TTACTCTCCT TATGAAAATA CTGGGGAATT GAAGAATTGA	720
TGAAGACCTA GAAATTGGCT TAAGACGGGC TAAGGCATTC TTTACAGTAT GTATCCTACA	780
GGTGCATTAA GCAAAGACAA TT	802

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTACTATTTT AGCATAAAAA TGCCCAAAGG GGGNGCCGTG TGTTTACTGA TTTTCAGGNT	60
AATGGACCAG GNAAATCAGC ATGAAAATAA AAAGAGAAAC AGATTATTTT AGCCATTTGT	120
CAGATTTATG CTATGCTTAA GGTAGAAAAT GAAAGGGATA ACAAATGTAT TTAGGAGATT	180
TGATGGAGAA AGCCGAGTGT GGTCAATTTT CAATCCTTTC CTTTCTATTA CAAGAGTCTC	240
AGACGACCGT CAAGGCTGTA ATGGAAGAAA CAGGATTTTC AAAAGCAACC CTAACCAAAT	300
ATGTCACCCT GCTCAATGAC AAGGCTTTGG ATAGTGGCTT AGAACTGACT ATTCACTCAG	360
AAGATGAAAA TCTGCGTCTG TCTATAGGTG CAGCTACTAA GGGGAGAGAT ATTCCGGAGC	420
TTGTTTTTTG GATAGTGCTG TTAAATACCA GATTTTGGTT TATCTTCTCT ACCACCAACA	480
GTTTTTAGCC CATCAGCTGG CTCAAGAATT GGTGATTAGC GAGGCTACGC TTGGTCGTCA	540
CTTAG	545

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GAGGTCAAGA TTGATTCCCA AGGTTNGAGG AATCTGCGGA ACCAGATTTA GAAGAAATCG	60
AGCGGTTACC ATGCTTGGCC ATGTGAATAC CGCCACCAGC CAAGACAAAG GCTGCAGTTG	120
TGGAAATATT AAAACTGAAA GACTTGTCCC CACCTGTACC ACAGTTGTCC ATAGCATCAT	180
GAATCTCAGT TGGAATATGC TGGGCATGTC CTCTCATGAC TTGGGCAATG GCTGTGCGTT	240

CTTCAGGTGT TTCCCCCTTC ATCTTAAGAG CTAAGAGGAG AGAAGCAATC TGCGCTTCAG	300
TTACACGCCC AGTTACGATA CGCTCAATGA CATCCGTCAT TTCCACACCT GATAAATTTT	360
CAAATTTTGC TAGTTTTTCA ATAATCTCTT TCATCCTAGT TTCCTCACTT TACAACCTCC	420
TCGATAAAAT TCCGAATAGA AGACAAGCCG TCTGGCGTTC CAATGCTCTC TGGATGGTAC	480
TGGAAGCCAT AAATCGGTAG GTTTTTATGT TGAATCCCCA TGATGGCTTG GTCATCAGTC	540
GAACGAGATC AAGCTTATCG ATACCGTNGA CCTCGA	576

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATTAAAGGGA GGCGAACATG GCCCAAGATA TAAAAAATGG AGAAGTAGAA GAAGTTCAAG	60
AAGAGGAAGT TGTGGAAACA GCTGAAGAAA CAACTCCTGA AAAGTCTGAG TTGGACTTGG	120
CAAATGAACG TGCAGATGAG TTCGAAAACA AATATTCTTC GCGCTCATGC AGAAATGCAA	180
AATATCCAAC GCCGTGCCAA TGAAGAACGT CAAAACCTTG CACGTTATCG TAGCCAGGAC	240
TTGGCAAAAG CAATCTTACC ATCTCTTGAC AACCTTGAGC GTGCACTTGC AGTTGAAGGT	300
TTGACAGATG ATGTGAAGAA GGGCTTGGGG ATGGTGCAAG AAAGCTTGAT TCACGCTTTG	360
AAAGAAGAAG GAATTGAAGA AATCGCAGCA GATGGCGAAT TTGACCATAA CTACCATATG	420
GCCATCCAAA CTCTCCCAGC AGACGATGAC CACCCAGTAG ATACCATCGC CCAAGTCTTT	480
CAAAAAGGCT ACAAACCTCCA TGACCGCATC CTACGCCAG CAATGGTAGT GGTGTATAAC	540
TAAGATACAA AGCCCGTAAA AAGCTCGCAG TAAAAATAGG AGATTGACGA AGTGTTTCGAT	600
GAACACAAGA AAATCTANCT TTTTACTCA GAGCTTAGGG CGTGTTTCGAT TCGGCAATTC	660
TGACGGTAG	669

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

CTAGTTCACC	ATTTCTATTT	AAATTCGGCT	CAACTACACC	GAAATATCAT	ATAAGGTAAA	60
GTTCCCACTA	AGAATCTCAG	AATGAAATTC	TTCACAACT	TCAGCGGTCA	AACTTAGCTT	120
ATCCAATTTC	AGACCGATAA	ACCCATACTT	CAGAGATACT	TCCTCTTGAA	ATTTAGAGTA	180
ACTCTTATTA	GACATTTGAT	GTATCGTTAT	CGGGCTATTA	GAAGGAGCCC	GATTTAAAAC	240
TTCTTTATTC	ATGAAATTTT	TCCTTCAAAA	AACAAAACAT	TCTATATACT	TAAATTTTAG	300
GGCAAGACTG	CCGTTCCACT	GACCACGCTC	CACTTGCCAG	CAAAGCTGGC	AGGTCCAGCC	360
TTACCCTAAA	TATAAATTAT	TTAATTTTTG	CCATTTCAAT	CAATTCTGCA	AAGGTCCCAA	420
GCTTTCTGGA	TTGAATTACC	TCATATTGGG	CATTCTGTCC	AAATGAAGCA	TTATTAATCA	480
CTTCAACCTC	ATAAAGGCCT	GGAGCAGAGA	AAACAGCTCC	AAATTTGGAT	TTATCGAAAT	540
GCATACCTAG	GTCACTCCAA	CAATCATTA	GGGTGGAGAC	TTTTATCCAG	CCTCGTTCCT	600
TCTTAGTAGA	AATAG					615

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CTACTGTAGT	TGGAACGTGT	GAAAAACAAG	GAAAAACAAA	GAAAGTTGTT	ACTTACAAGT	60
ACAAACCTAA	AAAAGGTAGC	CACCGTAAAC	AAGGTCACCG	TCAACCATAT	ACAAAAGTTG	120
TCATCAACGC	AATTAACGCT	TAATTTTAAG	GAGAACACAT	GATACAAGCA	GTCTTTGAGA	180
GAGCCGAAGA	TGGCGAGCTG	AGGAGTGCGG	AAATTACTGG	ACACGCCGAG	AGTGGCGAAT	240
ACGGCTTAGA	TGTCGTGTGT	GCATCGGTTT	CTACGCTTGC	CATTAACTTT	ATCAATTCTA	300
TTGAGAAATT	TGCAGGCTAT	GAACCAATCC	TAGAATTAAA	CGAAGATGAA	GGTGGCTATC	360
TGATGGTTGA	AATACCAAAA	GATCTTCCTT	CACACCAGAG	AGAAATGACC	CAGTTATTCT	420
TTGAATCATT	TTTCTTAGGT	ATGGCAAAC	TATCGGAGAA	CTCTTCTGAG	TTCGTCCAAA	480
CCAGAGTTAT	CACAGAAAAC	TAACACGGAG	GAAAACATTA	TGTTAAAAAT	GACTCTTAAC	540
AACTTGCAAC	TTTTCGCCCA	CAAAAAGGT	GGAGGTTCTA	CATCAAACGG	ACGTGATTCA	600
CAAGCGAAAC	GTCTTGGAGC	TAAAGCAGCT	GACGGACAAA	CTGTAACAGG	TGGATCAATC	660
CTTTACCGTC	AACGTGGTAC	ACACATCTAT	CCAGGTGTAA	ACGTTGGTCG	TGGTGGAGAC	720
GATACCTTGT	TCGCTAAAGT	TGAAGGCGTA	GTACGCTTTG	AACGTAAAGG	ACG	773

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CTGGATAATT	GGAGCAATTC	CTGATGCCAG	TTTGAGGTTA	CTGATAGGAT	TGTGGGCGAT	60
AGCCACTTGA	GAAGATGCCA	AGAGTTCAAT	TTCTCTCTCG	TTTAATTCGA	CCCCGTGAGC	120
AAATACGGAC	GGATGATCTA	AATAACCCAG	TTCTTCAAGA	AAAGCAAGGG	GGCGTTTGCC	180
GTACCGTTTG	AGGATAATTC	CTGACTCCTC	CTTGGTCTCC	GCCACATGGA	CATGGAGCGG	240
AATATTTAGC	TCTTTTGCCA	TTTCCAAACT	CGCTTCCAGC	AAGTCTCTAC	TGCAGCTATA	300
CGGAGAATGA	GGTGCTACCA	TAACCCTTGA	AATTTGGGAT	TTTTATATTT	TAAGATTTCG	360
TCTATGATGG	ATCGAGTTCT	GCTTATAGTC	TCAGCAGTTG	TTTCTGTCTC	TGAAGAAAAG	420
AGAGTCGGAG	AAAAATAACA	ACGCATCTTG	GAAGTTTTCA	CCACCTGATA	AATTTGCTGG	480
ATATCCACAC	CATTGGGATT	ATACATATCG	TTAAAGGTTG	TTGTTCTCTGA	CTGGAGCATC	540
TCTGTTAGGG	CTTCTTTGAC	CGCATTGGTA	GTCATGTCGG	GAGTAAACTC	AGATTCTGCT	600
GGCCAGATAT	AGTCATTGAG	CCATTTCATG	GAGATTGCTG	TCATCTCGGA	TCCCTCTCAG	660
ACCTGTCATT	GCAGAATGGG	TGTGACAATT	GACCAAACCA	GGCATAAGCC	AAG	713

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

CTAGAAAATC	TGCTTTTTTC	TCGAAAAGTT	TAATACTTGG	TACAATATTA	CGCTTGCTTT	60
GCTCGGCTGC	TCCAAGGGCA	ATTTTTTCTA	GTTTTTCAAC	TTTTTTACCC	AATTTCTTGC	120
CATCCCACCT	GGCAACTGAC	CAGTCTGCAG	GAAAGGCCCA	GATTTGGCTA	GCACCCAGTT	180
CGGTTACTTT	TTGAGCGATG	AACTCCAGCT	TGTCTCCCTT	GGGAAATCCA	GATGCGATGG	240
TCACTTGGAC	TGGTAGTTCC	ACATTGTCAT	TTAATTCTTG	GACCAACTCA	AACTGACGAT	300
TTTCCATATC	CAGCACGCGC	GCCAAGCGCT	TGATGCCATC	ATCAAAGACT	AAGGTAACCT	360
CATCCTCTTC	TTTCAAGCGC	ATAACCTGAA	ACATATGCTT	ACTGGTTTCC	TTGTCTCGA	420
TAGTGACAGG	AGAGATAGCA	CTGCCTTTTA	CAAAATACTG	CTGCATGCTA	GCCTCCAATC	480
ACACCAGAGA	TATCCTTGGT	TTTCTTAAAG	ACACAGGTAT	TCCATTCCCC	TTGAACCATG	540
TGAGTTTCGA	GGAAAAATCC	AGCTGATTCA	GCCGACTCGC	GCACCATGTC	CCACTTATGC	600
CTTGAATAAT	GCCACTCATG	ATCAGGTAGC	CTTCGTCCCT	AACCAAACGA	TAGGCATCGT	660
CTATTAGATG	AATGAGGATA	TCCGCCAAGA	TATTAGCCAC	AATCACATCT	GCCTCAATTT	720
CCACACCCTT	AAGCAAATCT	CCAGCCGCTA	CATGGATATT	TTCCATGCCA	GGGTTGAG	778

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

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CTTCCCAGAT TTTTTCGTTG ACTTGCTGTT CAATCGCACG CAATTCTTCA GCAGTTACAG      60
CTTGGAAGTG GGTAAAGTCA AAGCGAAGGA ATTCAACTTC GTTAAGAGAT CCTGCCTGTG      120
TTGCGTGGTT TCCAAGGATA TTGTGAAGGG CAGCGTGAAG CAAATGAGTC GCAGTGTGGT      180
TTTTTCATGAC ACGGTGACGG CGATTGCTAT CAATTGCCAA GGTATATTCT TGGTTCAAGG      240
CAAGCGGTGC AAGGACTTCA ACTGTATGAA GGGCTTGACC ATTTGGGGCT TTCTGAACAT      300
TGGTCACAGT AGCCACAACC TTACCTGACT CATCCAAGAT TTGTCCGTAG TCAGCTACCT      360
GTCCACCCAT TTCAGCATAA AATGACGTTT CCCGCAAAGA TAAGAGAGGC AGTTCCTTCT      420
GAAACAGCTT CTAATTCTGC ATTGTCCGCC ACGAATAGCT ACCAATTTAG AAGACAATTG      480
GCTAGCATTG TAGTTGAAGG CACTTTCTAC AGTGATGTTT TGAAGAGTTT CCATTTTGCA      540
TACCCATTGA GCCACCTTG ACAGCTGACG CACGCGCGCG TTCTTGTTGT TCTTTCATGG      600
CTGCTTCAAA ACCTTCACGG TCTACAGTCA TACCAGCTTC TTCAGCGATT TCTTCAGTCA      660
ATTCAACTGG GAACCCATAA GTATCATAGA GTTTGAAGAC ATCTGAACCA GCGATAACAG      720
ATTGACCTTT TTCTTCAAG TCTGCTACAA TGCCTTGGGC AAAGTGTTGA CCTTGAGTGA      780
AGGGTACGGG CAAATGATTC TTCTTCGCCT CTTAACGATT TTCTCAATAA AGTCACGTTT      840
CTCAAGCACT TCTGGGTAGT AGCTTTCCAT GATTTTTCCA ACAGTTGGAA CGAGTTTGTG      900
AAAGGAAAGG CTCGTTGATA CCAATTTT GACCCATGCA TAGAAGCACG ACGGAGAAGA      960
CGACGAAAGG ACATAACCAC GACCCTCCAT TTCCTGGAAG GGCACCATCC ACCGATGGCA     1020
AATGAAAGTG AACGGATGTT GGTCCGCGAA TGAACCTTGA AT                                1062

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(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 865 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CTCAAAGGTC	GCACCTGCAA	TACGACCCGC	TACAGGACCT	ACACTTGCTC	CATGCTTGGG	60
ACTATTGCCT	ACATAACTAC	CAAAGTCATC	AAATCCCAAG	ATAACATTGG	CAAAATTTCC	120
AGCCTTGTC	GGTGCGACAT	AGCGCAAGAT	AGTCGCACCA	TAAGTCATAA	CCTCAAGTTG	180
GTAGCCACCG	TCTGTCTCAA	ATCGATAGGC	CAAGACATCC	TCACCCTCAA	CATTTCCAAA	240
TACACGCTCT	GTGTATGCTT	TCATTCTGTT	CTCCTTTTAC	TATTTCTCTC	AAGCAAACAA	300
ACCATAGAAA	GCGTACTGAC	AATCTATGGT	TTATCTGATA	ATTTACAAAT	CCTCTTGTCA	360
AGAATTCATA	AACACTGTCT	TACTTTTGAT	ATTCGTGAAT	TATGACACCT	TGTACTACAC	420
GGTTTACTGT	ACCTGTAGGA	GACGGTGTAT	CTGGTTTATT	TTCTACCTTG	AGTGAAGTCA	480
ATAGGGCAAA	GAGTTGGGCA	TAAACGATGT	AAGGGAAGAC	ACGGTAAATA	TCATTCAAGA	540
CACCGCCACA	ACCAAGGGCC	ACTTCTTTGA	CATTTTCAAG	ACCAAAAGCT	TGATCACTCA	600
AAAGCACAA	ACGACGAGCA	ATCTGGTCAC	CAGCAACTTC	ACGAACCAAG	TCCAAGTCGT	660
ACTTACGAGT	GTAGTCCGTC	CTTGTAACAA	AGAACAAAAC	AACTGTATTG	TCGTTGATAA	720
GATATTTGGA	CCGTGACGGA	ACCAACTGGG	CTTTCATACA	TGGTCGCAAC	TTGAACAACA	780
GTTAATCCCA	AATCTTGAGC	TGAGCCTCAT	GAGCAGTCCA	AAGAAGACCA	GCGCCTAGAA	840
GAGACCGGTT	AAGTCTTAAT	CACAG				865

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 946 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TTTTGCTCCA	GTTGATAAGA	AAGGCTTGGT	CGATGTTGAG	GCGTTAGCAG	GTTTGATACG	60
GCCTGATACA	ATCCTCGTTT	CCCATCATGG	CTGTGAACAA	TGAAATCGGC	TCTATCCAAC	120
CNATTGAGGC	TATTTCAGAA	TTCTTGGCAG	ACAAGCCGAC	TATTTCCCTC	CACGTTGATG	180
CGGTTCAAGC	GCTTGCCAAA	ATTCCGACTG	AAAAGTATCT	GACAGAACGG	GTGGATTGCG	240
CGACCTTCTC	GAGTCATAAA	TTTCATGGTG	TCCGTGGTGT	TGGCTTTGTC	TATATCAAAT	300
CTGGCAAGAA	GATTACACCT	CTTCTTACAG	GTGGTGGCCA	GGAGCGAGAT	TATCGTTTCGA	360
CAACTGAAAA	TGTGGCAGGG	ATTGCAGCGA	CAGCCAAGGC	TCTCCGTTTA	TCTATGGAAA	420
AGCTAGATAT	CTTTAGGAGC	AAGACTGGGC	AGATGAAGGC	AGTGATTAC	CAAGCTCTTC	480
TGAACTATCC	GGATATTTTT	GTCTTTTCAG	ATGAGGAAGA	CTTTGCACCT	CATATTCTGA	540
CTTTTGGAAT	CAAAGGTGTT	CGAGGTGAAG	TCATCGTTCA	CGCCTTTGAA	GACTATGATA	600
TTTTTCATCTC	AACAACCTCA	GCTTGTTTCAT	CTAAGGCAGG	AAAACCAGCC	GGTACCTTGA	660
TTGCCATGGG	AGTGGACAAA	GATAAGGCCA	AGTCAGCTGT	GCGTCTTAGC	CTAGACTTGG	720
AAAATGATAT	GAGTCAGGTC	GAGCAGTTTT	TGACCAAGTT	AAAATTGATT	TACAATCAAA	780
CTAGAAAAGT	AAGATAGGAG	CATTCATGCA	GTATTCAGAA	ATTATGATTC	GCTACGGAGA	840
GTTGTCAACC	AAGGGTTAAA	AACCGTATGC	GTTTCATCAA	TAAACTTCGT	AATAATATTT	900
CGGACGTTTT	GTCTATCTAT	ACCCAAGTTA	AGGTAACAGC	AGATCG		946

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

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CTTGCTCGTA ACAGGTGCTA TCCTTGGTGT CAATGTTTAC ATCTTCTCAC CAAAAGAACT    60
CTTCCCAGAA AAAGAAATCG TTGAATTGGC AGAAGGATTT GCTAAAGAAA GTGGCGCACA    120
TGTTCTCATC ACTGAAGATG CTGATGAAGC AGTTAAAGAT GCAGACGTTT TTTACACAGA    180
CGTTTGGGTA TCAATGGGTG AAGAAGACAA ATTCGCAGAA CGTGTAGCTC TTCTTAAACC    240
TTACCAAGTC AATATGGACT TAGTTAAAAA AGCAGGCAAT GAAAACTTGA TCTTCCTACA    300
CTGCTTGCCA GCATTCCACG ATACTCACAC TGTTTATGGT AAAGACGTTG CTGAAAAATT    360
TGGTGTAGAA GAAATGGAAG TAACAGACGA AGTCTTCCGC AGCAAGTACG CTCGCCACTT    420
CGATCAAGCA GAAAACCGTA TGCACACTAT CAAAGCTGTT ATGGCTGCTA CACTTGGTAA    480
CCTTTATATT CCTAAAGTAT AATTTTAGAT AATAAACCGT CTACCAACAG CTATGAGGGC    540
TGCGACTAAT AG                                     552

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(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

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CTAAAAAAG TCAAGTAGAA AACGAATATT CTAATTAACT TGCACGAAAT TATTTTTCAC    60
GAATGACTTC GACCTTATAT CCATCAGGGT CTTTGACAAA GTAATAGTTT GGTGCAGTTC    120
CTGGTAGACC ATTTGGCTCA GTCAC TTCAT AGCCTTTTGT ACTGTGCTCT TGATGAAGTG    180
CCTCAAGATC AGGTGTACTG AGGGCGATAT GGGCAAACCC ATCACCACCC ACATACGGAC    240
CGTGATCGTA GTTATAAGTC AACTCCAAC CATAGTCATC ACCCTCAAGA CCTAGATAGA    300
CAATCGTGAA GGCATGGTCT GGAAAATCTC TGCGACGCAA TTCTTTAAAA CCAAAGCAT    360
CTTGATAAAA TGCAATTGAT TTTTCAAGAT TTTCTACTCG TAAGCAAGTG TGTAGCATTT    420
TTGAAGCCAT ATCTTTCTCC TTTATTTTAA AAAAGACTGG ACAATCCTGT TCCAGTCTCA    480

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TCAGTTGTGA TTTACCAAGT TTTGCTTTAG CT

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CTGGACCACA CTATTTTCTG TGTGGCTAT CGTGTCATGC AAAAGGATCT AGAAGGGACG	60
CTGGATGCTG AAAAAGCTCA GGCTGCTGGT GTTCCGTTTCG GCGCGCTTTT TGGTAAAATC	120
AAAAACGGCC AGGATCTTGT TTTGGAAGAC GGAAGTAAA TCAAGGCAGC AGACTATATC	180
TCAGCGCCAC GTCCAGGTAA GATTATCACT ATTTTAGGAG ACGTTCGAAA AACGGATGCC	240
AGTGTGCGTC TGGCTGTCAA TGCAGATGTC CTAGTTCATG AGTCCACTTA TGGCAAGGGT	300
GATGAAAAAA TTGCTCGTAA CCATGGTCAC TCAACTAATA TGCAAGCTGC ACAAGTAGCG	360
GTAGAAGCAG GTGCCAAACG CCTCCTACTC AACCATATCA GTGCGCGTTT CCTCTCAAAA	420
GATATAAGCA AACTCAAGAA GGACGCTGCC ACAATTTTTC AAAATGTCCA TGTGGTCAAA	480
GACTTGGAAG AAATGGAAAT CTACCAGTCA CAGAAAGGAT AAGTATGCCT ACTATTCTCC	540
ATTAACCGGA A	551

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CCGTCATTAT ACCTTTGTCT ATGAAAATGA AGACCTAGTC TATGAGGAGG AAGTCTTATG	60
ATACAGCCAG CAAGTTTAGA AGAATTAGCA TCTTTAGTGG AAAAAGCGGG CAAGAAGGTC	120
TTCCTTTTTG TGGCAGACTG GTGTGGCGAT TGTCGTTATA TTTATCCTGC CTTACCAGAG	180
ATTGAGGAGA CCAATCCAGA GTTCACCTTT ATTCGAATGG ACCGAGATCA GTATATGGAT	240
TTGGCCAAAC TCTGGGATGT TTACGGAATT CCTAGCCTTG TTGTTCTAGA AAAGGACAAG	300
GAAATTGGTC GTTTTGTCAA TCGCGACCGT AAAAGTAAGG AGCAAATTAA CGATTTTTTA	360
GCAGGATTGA AATAGGAGAA AAAGGAAACA ATGATTTTTTA CGTATAACAA AGAACATGTC	420

GGTGATGTCC TTATGGTCAT CGTGAAAAAT AGCGGAGATG CCAAAGTCAA TGTGGAACGC	480
AAAGGCAAGG TAGCCCGTGT TTTCTCTCAA GAAAATGGGG AAACAGTAG	529

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CTAGGATAGA CCGCTTTTFA GCATTTATCT AAGCATTCCA GAGTACATGT ATCTTGCATG	60
TGCTCTTTCT TTTGGGGTTG AAACGATAGG AGAAGGAAAT GTTAGAATTG CTTAAATCAA	120
TCGATGCTTT TGCTTGGGGA CCGCCCTCT TGATTTATTG GTCGGAACAG GGATTTACCT	180
AACCATGCGG CTAGGACTCT TGCAGGTTTT GCGTCTGCCC AAGGCCTTTC AGCTTATTTT	240
TATCCAGGAT AAGGGACATG GTGATGTATC CAGTTTTACA GCTTCTTG TG TAACAGGCCC	300
TTGGGCATTC AAAGTGGTTG GGAAACAGGG AAATATCCAT TAGGGAGTTG GCGACGGCTA	360
TCAAGGTTGG TGGACCAGGA GCTCTATTTT GGATGTGGAT GGCGGCTTTC TTTGGAATGG	420
CTACCAAGTA TGCAGGAAGGA CTCTTGGCCA TCAAATACCG CACCAAGGAC GACCATGGTG	480
CAGTAGCGGG AGGTCCCATG CATTATATCC TTCTAGGGAT GGGAGAAAAG TGGCGACCAC	540
TTGCTGTTTT GTTTGCAGTA GCAGGAGTAT TGGTTGCTCT CTTGGGAATC GGAACCTTCA	600
CCCAAGTCAA CTCGATTACA GAATCTATCC AAAATACAAC GACGATTTTCG CCAGCCATCA	660
CAG	663

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 727 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CCTTGACCAC CAATTCTTCA CCCGATATGA TGCGCCCTGC TCGCTGAGCA AGCCCCAAGA	60
GATTACTTAT CTTTTGCTTA TTCAAGTCCC AACTCTCTTC TTTTCACTTT GTGATCCACA	120
TAAGCGATCA ACTCGTCATA AAAGCTTTCT TCCACTTCCA TGCTAAAGCT GCGGTTAAAG	180
ACCTTCTTCT TTTTCGCCTC TAGGGCTTCT GCATTGTCTA GTTTGATATA AGCGCCGCGG	240

CCATTGGCCT	TGCCCCGTAGG	ATCAATAAAG	ACTTGTCCTT	CCTTGTTCTT	GACAATGCGG	300
AGCAAATCAC	GCTTATCAAT	CACTTCGTTA	GACACAACAG	ACTTGCGCAA	AGGGATTTTT	360
CTTGTTTTCA	TCTTTCCCTC	CTCTAGCAGC	TTTTATTCTT	CTACAGTATC	GTTTTCTACT	420
TCCAACTCTA	CTGAAGCAGC	GTCTTCCATG	GCTTCAAATT	CGCTAGCAGA	CTTGATATCG	480
ATACGGTAAC	CAGTCAAGTG	AGCCGCCAAG	CGCACGTTTT	GTCCACGACG	ACCAATGGCA	540
AGAGAAAGCT	TGTTATCTGG	AACAACCACC	AAGGCACGTT	TGCTGTCGTT	TTCATCAAAG	600
ATAACTTGGT	CAACCTCAGC	AGGAGCGATG	GCATTGTAGA	TAAATTCAGC	TGGATCTGCT	660
ACCCACTCGA	TAACATCGAT	ATTTTCTTCG	ATTGGTACCA	TGCGGTCATT	TTTAGCATCG	720
TAACGAG						727

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CTAATGTAAA	TCTATGGGAT	AAACGTTAGC	TTCTTTTAAT	AGATTATTAA	GCAATTTTTT	60
AAAACAACCTC	ATCAAACAAA	CTCAACTGGT	TATCTCTGGC	ATATTTCCAA	GAATACCCAT	120
CTCATCCATC	TTTTCAACCA	AGGTTGATGA	GAGTCCACCA	CGCTTGCGTA	GTTCTGTTTT	180
AGAGAGGAAT	TCTCCCTCTT	CACGCGCCCG	CACCAGTTGC	TTGGCAACGT	TCTCCCCCAG	240
ACCATCCATT	GCTACAAATG	GTGGGATAAG	GGTATCCCCG	TCGATGAGGA	ACTCTGTCGT	300
CTGACTACAG	TAGAGATCTA	ATTTACCAA	CTTGAAACCT	CGTTCCCACA	TCTCATTGAC	360
AATCTCAAGA	GTTGTATAGA	GATCGATTTC	CACATTAGAG	GCTTCATTGT	TCTTCCGTTT	420
TTCAGAGATT	TCTTCCATTC	TGCGCTTGAT	GACCTCCAAG	CCCGCACCCA	TGGTCTTGAT	480
ATCAAAAGCC	TTAGCACGAA	TGGAGAAGTA	AGCACAGTAG	TAATAAATAG	GATGGTGAAC	540
CTTGAAGTAA	GCTACACGCA	AGG				563

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 647 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

CTAACTTCAA AAGCTTTTAG AATATCTTCT TGACTAATCA TATGATTACC GCCCAAGGTT	60
AAGTTTTCCT AAATAGAGCC ATTAAAGATA TAGGCTTGTT GGGGTAGGTA ATTAATATGA	120
CGGCGCAAGA CTTTTTTTAT CAATGTTTTT AATATCCTGA TGATTGATGG AAATATGCCC	180
TTTGTAGGGT TCAAAGAAAT TGACAATCAT TTTGGCTAAA GTTGTTTTAC CAGAACCACT	240
AACTCCAACCT AGGCTAACCT TATCTCCTTG TTTAATCGTG AGATTAAATAT CTGTTAAGGT	300
ATCTCGTCCA AAACCATACT TATAAGAAAG GTCATCAAAT TCAATATCGC CCATCAAAAA	360
ATGTGAATGA ACAGGGTTTT CTTGAACTTG AAATTCAGAT TCGACTAGAT AGACTTCGTT	420
CAAACGGTTA TTAGCGACCT TCGCAGATTG GAGTTTGTT TGGAGGTTGA TAATATTTTC	480
CATAGGAGTT GTAAAGTAAG AAAGAAGTGT GTTAAAGGTA ATCAGCTGAC CGATAGAAAT	540
TTTACTCGAC ATGACTAATT GAGCGCCAAA CCATAGGATA AGGATATTCA GAACTAATTT	600
TGTTTCCCCT GCTTTAAACT CGTTTGTAAT ATAGAATATT TACTGAG	647

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CTATCCTNGA ACCAATGATG CTTGTAACAA TCACTGTTCC AGAAGAAAAC CTTGGTGATG	60
TTATGGGTCA CGTAACTGCT CGTCGTGGAC GTGTAGATGG TATGGAAGCA CACGGTAACA	120
GCCAAATCGT TCGTGCTTAC GTTCCACTTG CTGAAATGTT CGGTACGCA ACAGTTCTTC	180
GTTCTGCATC TCAAGGACGT GGTACATTCA TGATGGTATT TGACCACTAC GAAGATGTAC	240
CTAAGTCAGT ACAAGAAGAA ATTATTAAGA AAAATAAAGG TGAAGACTAA TCCGTCCTCA	300
CTCTAGAAGG AAGTCACTTA GTGGCTTCCT TTTGTCTTTA GAAAATACCT CTAAATATGG	360
TAAATAGTA GAAGAATAAT GTGAGGAAAA TGAATGTCAA ATAGTTTTGA AATTTTGATG	420
AATCAATTGG GGATGCCTGC TGAAATGAGA CAGGCTCCTG CTTTAGCACA GGCTAATATT	480
GAGCGAGTTG TGGTTCATAA AATTAGTAAG GTATGGGAGT TTCATTTCCG TATTTTCTAA	540
TATTTACCTA TTGAAATCCT TTTTACAATT AAAGAAAGTT TGAGCGAAGA ATTTCCTNAG	600
AANGCCATCA	610

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TATAAGCATA	GTACCAGTTG	CCATTGACCT	GGAACCAACT	GTCTTCATAT	CTCCATTACT	60
GCATTTAGGT	AGTACCAAGT	TGAACCATCT	TGATACCAAC	CAGTTGCCAT	TGCTCCTGAT	120
GAACGGAGAT	AGTACCATTT	GTTCCCAAGG	TTTGCCAAC	CTGTTTTCAT	ATCGCCATTT	180
GGCTGGTCTA	AATAATACCA	AGTGGTACCT	TCCTGATACC	AACCAGTTGC	CATTGCTCCT	240
GATGAACGGA	GATAGTACCA	TTTGTTCCTA	AGGTTTTGCC	AACCTGTTTT	CATATCGCCA	300
TTTGGCTGGT	CTAAATAATA	CCAAGTGGTA	CCTTCCTGAT	ACCAGCCAGT	GGCCATTGCT	360
CCTGAGGAAC	GGAGGTAGTA	CCACTTATTA	CCTAGATATT	GCCAACCTGT	TTGCATAATA	420
CCAGTTGTTG	GATCTAAATA	GTACCAAGTC	AAATCATCGT	TTATCCACCC	CGCACGTCTT	480
TCACCACCAA	GGTAGTTTTC	TCCATTAATT	TCCGTCTTAG	CTAGATAATA	CCAGTAGACT	540
GATCATAAAG	CCAACCTGTC	TCTAAAGAAT	GATTTTGATT	AAAGTAATAG	TTCGTATAAT	600
AACGNTTCTC	TTCTTTATCT	TCTGAATCTT	CACGTTTTTC	CCCGTACTTT	CTTCCAACAC	660
TGTCTTTAGT	TTTAATCTCT	AATGTTTTCC	AACCAACAAA	CTCTTGTAGC	ACTCCATTTT	720
TATCGAAGTA	GTACCACTCT	GAATTTGGAA	AACCTTCTAA	TCTCATACCA	TTTGGGTAAG	780
GACCAATTGT	ACTACCTTTA	GATGGAAACG	GGATATATTG	CCAGCCGACA	ACCATCTCTC	840
CAGATAGAGA	ATCAAAATAA	TAGTACTTAC	CATCAATCAC	TCGCCAGTAG	GTTTCTTTGA	900
GGTCCCCCTT	TTTGTAATAG	GTTCTACCGT	TTTCTTGGAC	AAACTGCCAT	CCTTCAGAGT	960
TATCTGCAAA	TACTGTATTC	GTAG				984

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 842 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CCTCGTTATG	CAGATGAACG	TTATTTCTTG	TCAAAGAGTC	ACAAGAATTT	TGTTGATCGT	60
AATCTTTTTA	TTACCATTCG	TGACAAGGAA	ACCACCTGTA	TCAAGCCTTA	TCAGCAGGAT	120
TTGGATTTGC	CACATGGTCT	GGCCTTGGAT	GTTTTGCCTT	TGGATTATTA	TCCGAAAAAT	180
CCAGCTGAGC	GGAAAAAACN	GGTTCGTTGA	GCCTTGATTT	ATTCACCTCT	TTGTGCGCAA	240
ACTATTCCAG	AAAAGCATGG	TGCTCTCATG	AAATGGGGAA	GTGCGATTTT	ACTGGGTTTG	300

ACTCCAAAAT CTCTCCGTTA TCGCATCTGG AAAAAAGCTG AGAAAGAAAT GACTAAGTAT	360
GATTTGGCTG ATTGTGATGG CATTACAGAA TTATGCTCAG GTCCTGGCTA CATGAGAAAC	420
AAGTACCCAA TCACATCTTT TGAAGACAAT CTTTTCTTGC CATTTGAAGG AACAGAGATG	480
CCTATTCCAA TCGGCTATGA TGTCTATCTC AGAACTGCTT TTGGGGATTA TATGACGCCT	540
CCACCAGCAG ACAAGCAGGT ACCGCATCAG GATGCTGTCA TCGCTGATAT GGATAAGTCT	600
TATACAGAAAT ACAAGGGAGA ATATGGTGGC TAAGAAAAAA ATCTTATTTT TTATGTGGTC	660
TTTTTCTCTT GGAGGTGGTG CAGAGAAGAT TCTATCAACC ATTGTTTCAA ATCTGGATCC	720
AGAAAAGTAT GATATTGATA TTNTTGAAAT GGAGCACTTT GACAAGGGAT ATGAATCTGT	780
TCCAAAGCAT GTACGCATTT TAAAATCCCT TCAAGATTAT CGCCAAACCA GATGGATACG	840
AG	842

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 749 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CTGGCAAATA CAAGGTGACG ATCATTGGTA AATCAGCCCA CGGTGCTATG CCTGCTTCAG	60
GTGTCAATGG TGCGA ¹ CTTAC CTAGCCCTCT TCCTTAGCCA GTTTGACTTT GCTGGTCCAG	120
CCAAAGAATA CCTTGACATC ACTGGTAAAA TTCTCTTGAA CGACCATGAG GGTGAAAGTC	180
TCAAGATTGC TCATGTGGAT GAAAAGATGG GTGCCCTTTC TATGAATGCA GGCGTCTTCC	240
GCTTCGATGA AACAAGTGCT GATAATACCA TTGCCCTCAA CATCCGCTAT CCAAAGGAA	300
CAAGTCCAGA ACAAATCAAG TCAATCCTTG AAAACTTGCC AGTTGTTTCT GTTAGCCTGT	360
CTGAACACGG TCACACGCCT CACTATGTTG CCAATGGAAG AATCCACTTG GTTGCAAACC	420
TGGTTGAAAT GTCTATGAAA AACAGACAGG CCTTAAAGGT CATGAACAAG TCATCGGTGG	480
TGGAACCTTT GGTGCTTGT TAGAGCGCGG AGTTGCCTAT GGTGCTATGT TCCGAGACTC	540
AATTGATACC ATGCACCAAG CCAATGAATT TATTGCCTTG GATGATCTCT TCCGAGCAGC	600
AGCAATTTAT GCCGAAGCTA TTTACGAATT GATCAAATAA AACGATAGAA GTCTGAGATC	660
TTATGCTTGG ACTTCTTTTT GGAGGGAAAG TAGATGTCTC AAATCGAAAG AATCAAACAG	720
GCTATCATGG CGGATTCACA GAATGCCAG	749

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

CTGGATGAAT TGCAGAAGCG CAACCTACTG GGATTTGTCT TCCAAGATTT TCAACTATTT	60
CCTCATCTAT CAGTTCTGGA AAATTTGACT TTATCGCCTG TGAAGACCAT GGGAATGAAG	120
CAGGAAGAGG CTGAGAAGAA GGCGAGTGGA CTCTTGGAAC AGTTAGGACT AGGAGGACAC	180
GCAGAGTCCT ATCCTTTCTC ACTATCTGGT GGGCAAAAGC AGCGGGTGGC TTTGGCGCGT	240
GCTATGATGA TTGACCCAGA AATCATTGGC TACGATGAAC CAACTTCTGC CCTGGATCCA	300
GAATTACGTT TGGAGTGGA GAAGCTAATC TTGCAAAATA GGGAAGTTGG GATGACCCAC	360
ATTGTGGTTA CCCATGATTT GCAGTTTGGC TGAAAATATC GCACATGTTA TTATTGAAAG	420
TAGAACCTCA AATAGGAAGA AAAATGGATT GAAAAAATGG ATGCTTGTAT TAGTCAGTCT	480
GAAGACTGCC TTTGTTCTTA GTA	503

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

CTGGAGGGCA TTCAGTATTA CTTGAATAGA GGAAAACATC ATCTCCCTTA TGTTCTCAAT	60
ATTGGATTTC CTGGTCAGAA AAATGACCTC TTAATCCTTC GGCTAGATTT AGCTGGAATT	120
TCAATCTCTA CTGGCTCAGC CTGTACTGCA GGCGTTGTCC AATCCAGCCA TGTTCTTAAA	180
GCCATGTATG GCGCAAATTC AGAACGCTTG AAGGAATCCC TTCGCATCAG TTTGTCGCCA	240
CAAAATACCG TTGAAGACCT ACAAACCCTC GCAAAAACCT TAAAAGAAAT TATCGGAGGT	300
TAGCCATATG GCATTTGAAA AAATCATTCA GTTAAAAAAT TGTCGTTACG ATTACACTCT	360
TAGCCCTTCT GTTAAAAAAT TCACCCTCAA AGATAACACC TTTTTTGAAA CTAAGGTTGG	420
TAACTATGAA CTGACTCGCC TTTTGGAATA AGTGCCAAAC AGCGGTGAAG GCTTCCAAC	480
CAAAATCATC ATTAACAAGG AACTTACAGG GGCTAAAATC AATATCACTG ACAAGTTTGG	540
CCTTCGTCTA GTTGATATTT TCAAATCAGA AGACCACCAT ATTCATCAGG AAAAATTCTA	600
CTTCCTCATG GATAG	615

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 954 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CTGCAATGGT	TAGCGAGGAT	GGTGAAATAG	AGGAGCCTTA	ACTATTTTGA	GGAATCCAAG	60
CTGACAGGAC	TGGTATGTCT	GCTCTTTGGC	TCTGAAGGCA	GACTATACCA	GCTGGAAGTT	120
TGACAGATGT	GGCACGTGAG	AATTATTGGA	GGCNTTGACN	TANTCAGAGG	ATTCTCTCTT	180
GATATTGGGT	TTGGCAGAGT	TGGATAGTGA	GTTGGAAAAT	TACCAAGCGG	TTATTCAAGC	240
CTATGCCCAG	TTAGATAATC	GCTCGATTTA	TGAGCAAACG	GGCATTTCCT	CCTATCAACG	300
AATTGGCTTT	GCCTATGCTC	AGTTAGGGAA	ATTTGAAACG	GCTACTGAGT	TTTTAGAAAA	360
AGCCCTGGAG	TTAGAATACG	ATGACTTAAC	AGCTTTTGAG	TTGGCCAGTC	TTTATTTTGA	420
TCAAGAAGAA	TATCAAAAAG	CCACCCTCTA	CTTTAAGCAG	CTTGATACCA	TTTCTCCTGA	480
CTTTGAAGGC	TATGAGTATG	GGTACAGTCA	GGCTTTACAT	AAGGAACATC	AAGTTCAAGA	540
AGCCCTGCGT	ATCGCTAAGC	AAGGATTAGA	GAAAAATCCC	TTTGAAACTC	GCCTCTTGCT	600
AGCTGCTTCA	CAATTTTCTT	ATGAATTGCA	TGATGCTAGT	GGTGCAGAAA	ATTATCTCCT	660
TACTGCAAAA	GAAGACGCTG	AGGATACAGA	AGAAATCTTG	CTTCGTTTAG	CCACTATTTA	720
TCTGGAGCAG	GAGCGTTATG	AGGATATTCT	AGACTTGCAG	AGTGAGGAGC	CAGAAAATCT	780
TTTGACCAAG	TGGATGATTG	CTCGTTCTTA	TCAAGAAATG	GACGATTTGG	ATACTGCTTA	840
TGAGCATTAT	CAAGAGTTGA	CAGGAGATTT	GAAGGACAAT	CCAGAATTTT	TGGAACACTA	900
TATCTATCTC	TTGCGTTGAA	TTGGGACATT	TTGAAGAAGC	AAAATCCCAT	GCTC	954

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 564 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

CTATGAAACA	TTTTGATACT	ATTGTCATCG	GTGGGGGACC	TGCTGGTATG	ATGGCTACGA	60
TTTCCAGTAG	CTTTTATGGA	CAGAAAACCC	TCCTCATCGA	AAAAAATCGG	AAACTTGGA	120
AAAAATTAGC	TGGGACTGGT	GGGGGACGTT	GCAATGTGAC	CAACAATGGT	AGCTTAGACA	180
ACCTGCTAGC	TGGAATTCCT	GGAAACGGAC	GCTTTCTTTA	CAGTGTTTTT	TCCCAGTTCG	240
ATAATCATGA	CATCATCAAC	TTTTTTTACAG	AAAATGGTGT	TAAACTTAAG	GTCGAAGACC	300
ACGGACGCGT	CTTTCAGCC	AGTGACAAGT	CTCGGACTAT	TATCGAAGCT	TTGGAAGAA	360
AAATCACTGA	ACTAGGTGGT	CAAGTTGCTA	CTCCAAATAG	AAATCGTTTC	TGTTAAAAA	420
GTAGATGACC	AGTTTGTCTT	TAAGTCAGCG	GATCAAACCT	TCACTTGTGA	GAAACTCATT	480

GTCACAACAG GTGGTAAGTC TTATCCTTCG ACTGGTTCGA CTGGTTTGG TCACAATGCT 540
CCGCCATTTA AGCATACCAT CACG 564

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CTCCGTGGTC	TTTTGGTTTG	CTACGGGATG	TAGGCAAAAG	GCAAGTCCAT	TTTATCAGCA	60
ATAATGGCTC	CGTGTGGAAT	CCCTGCTGTT	GCAGTTCCTG	CAATCACTTC	TACTTCAGGA	120
AAGGCTTCTT	TGATAGCTTC	CACAAAACCA	TTTTCAATTA	GGGTACGAGT	TTCTGGATAG	180
GCTAGTGTC	CACGATTATC	AGTGTAATC	GGTGACTTGA	TACCAGATGC	CCAAGTGAAG	240
GGTTCCTCTG	GTTTGAGGTA	AACGGCTTGG	ATTTTCAAGA	GGTGGCTAGC	GATATCTTTA	300
GCAAGTGTC	TGGTATTCTC	CTTTTATTTT	TCTAATCTAG	TTCTTTAATT	CCAGTCCTGT	360
GTCCATTCAT	CCTTGATGGC	ATGATAAGCT	GCAACAGGAT	CCTCAGCTTG	GGTAATGGGA	420
CGTCCCCTA	CGATATAGTC	ACTGCCGATT	TGATAGGCAT	CAGCAGGTGT	CATGACTCGT	480
TTTTGATCTC	CAACTGCAAC	ACCAGCTGGA	CCAATCCCTG	GTGTCCCGAC	AGATAAAAAT	540
CTGGATTGGT	AGCCCTGCTT	GATGACTTTG	TCACTTCCCT	GAGCCGAGCC	AAACCAACAC	600
CCATCCCAAA	GCCCAAGCTT	CAGCTGTCTT	CCTTGGCATA	GTTGAATCCA	C	651

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 602 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CTTAGTATCT	AGAAAAGGAG	AAATAAAATG	GTAAAGTAT	TAGCAGCGTG	CGGAAATGGA	60
ATGGGTTTCAT	CAATGGTTAT	CAAGATGAAG	GTTGAAAATG	CTCTCCGTAA	GCTTAATCAA	120
ACAGATTTTA	CAGTCAATTC	ATGCAGTGTC	GGTGAAGCTA	AAGGTTTAGC	AGTAGGATAT	180
GACATCGTAA	TCGCTTCTCT	TCATTTGATT	CAAGAATTGG	AAGGGCGAAC	TAATGGGAAG	240
TTAATTGGGC	TTGATAACTT	GATGGATGAT	AAAGAAATCA	CCGAAAAACT	CAGTCAAGCA	300

ATACAGTAAA AGGTTGGAGG GGGCTGGACA CAAACTGAGA GTTATCGTTT CTGTCCTTCT	360
CCCTCTTTAA ATAAAGGAGG CAGATATGAA TTTAAAACAA GCTTTAATTG ACAACGACTC	420
GATCCGACTA GGTTTAGAAG CTAACGAATG GAAAGAAGCA GTCAAGGTAG CAGTAGATCC	480
CTTGATTGAA AGTGGGGCAA TTTTGCCAGA GTATTACGAT GCTATCATTG AATCGACTGA	540
AGAGTATGGG CCTTACTATA TCTTGATGCC AGGTATGGCT ATGCCCCACG CTAGACCTGA	600
AG	602

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ATTGGAATT TTTGCAACTG CAATTGGTGC CCTCAGTAAT CTATAAAATA GATTCAAGAA	60
AATTTAGTGA CTGGGATTTT CCAGCCCTTT TTTAAAGTGA GAAGAAATAA TGAGTATGTT	120
TTTAGATACA GCTAAGATTA AGGTCAAGGC TGGTAATGGT GGCGATGGTA TGGTTGCCTT	180
TCGTCGTGAA AAATATGTCC CTAATGGAGG CCCTTGGGGT GGTGATGGTG GTCGTGGAGG	240
CAATGTGGTC TTCGTTGTAG ACGAAGGACT ACGTACCTTG ATGGATTTCC GCTACAATCG	300
TCATTTCAAG GCTGATTCTG GTGAAAAAGG GATGACCAA GGGATGCATG GTCGTGGTGC	360
TGAGGACCTT AGAGTTCGAG TACCACAAGG TACGACTGTT CGTGATGCGG AGACTGGCAA	420
GGTTTTAACA GATTTGATTG AACATGGGCA AGAATTTATC GTTGCCACG GTGGTCCGTG	480
GTGGACGTGG AAATATTCGT TTCGCGACAC CAAAAAATCC TGCACCGGAA ATCTCTGAAA	540
ATGGAGAACC AGGTTTCAGGA ACGTGAGTTT ACAATTGGAA CTAAA	586

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TTCGACAATC TTGCCCNGA TCCAAGACAA CCACTTCTCT GTCCGCTCAG CAATAGTCAA	60
GCGGTGAGCA ATGAAAATCA AAGGTCTTGT CCAAAGCCAT GAGATAATGG ACAATCCGTT	120

TTTTTGTCAA AATATCCAAA CTGTTAGTCG CCTCATCCAA AATCAAGACC GGCGCATCTG	180
TCAAGAGAGC ACGCGCCAAA GCGATTCTCT GACGTTGACC ACCTGAAATC CCTGCCCCAT	240
CCGAAGTCAA TTCTGTCTGG TAAATTTCAA GGTGGCATGG CGGCTTCGAG ATATTCTCT	300
TCGGAATCTC TGAACCAAAT TCGGACCGGC CCGTTAAAGA TATCTTCCCT GTGTCGTCCC	360
CTCCCTTGGC TCCCAAAGA AGATTCTCCA AAATCGTTCC GTTAAAGACA TAGGGCTGTG	420
GAGGCAGATA GATGATGTAC TGGCGTAGGG CTTTTTTATC AATCTGATTG AGATTGACAC	480
CACCCAGACT AATCTCCCTT TGACTTGGGT CGTAAAAATT AACCATCATC TTGGCCAAAG	540
TCGTCTTACC TGACCCTGAA ATCCCCACAA AAGCCACCTT AGACCCTTGG GGAACGGTTA	600
AATTGATATC CGACAAGACG TCTCGACCAT AGCCATACTT GTAATGAACC TGCTTGAAAG	660
TCATCTCTCC CTTTCATCAAG	680

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

CCAATTTGGA TTTGCGAGAA GGCGTTATTA TTTCAGATGC TGGTTCGACC AAGTCAACCA	60
TTGTGGATGC GGCGGAGCAG TATTTGGCTG GCAAGTCTGT TCGCTTTGTC GGGGCCCCATC	120
CCATGGCTGG TAGTCACAAG ACAGGGGCTG CTTCGGCAGA TGTCAATCTT TTTGAAAATG	180
CCTATTATAT CTTTACAACC TTCCAAAGCC CTGAACAAGT CAAGGACAAC GCTTAAAGGA	240
AATGGGAAAG GATCTGCTTT CCAGGTCTTC ATGGCTCGTT TTATCGAGAT TGATGCCAAG	300
GAGCATGATC GTGTCACTTC TCAGATTAGC CATTTTCCTC ATATTTTGGC TTCTAGTCTC	360
ATGGAGCAGA CTGCGGTCTA TGCTCAAGAG CATGAGAATG GCAAGGCGCT TTGCGGCAGG	420
TGGTTTTTCGA GATATGACCC GAATTGCGGA AAGCGAGCCA GGAATGTGGA CCTCCATTCT	480
CTTGTCCAAT AGCGAGACCA TTCTGGATAG AATTGAGGAT TTCAAGGAAC GTTGGGAAGC	540
GATTGGTCAG GCCATTAGTA AGGGAGATGA AGAGCAAATT TGGAACCTTT TTAACCAAGC	600
G	601

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

CTGGCTCATC	AGGGGCAGGA	TATTTATGAT	TTCCCTCGTG	CTATGATTAA	GGAAGATAAT	60
CTGGAGTTTT	CATTCTCTGG	TTTGAAATCT	GCCTTTATCA	ATCTTCACCA	CAATGCCGAG	120
CAAAGGGGAG	AAAGTCTGTC	TACAGAGGAT	TTGTGTGCTT	CCTTCCAAGC	AGCTGTACTG	180
GATATTCTCA	TGGCAAAAAC	CAAGAAGGCT	TTGGAGAAAT	ATCCTGTAA	AACCCTGGTT	240
GTGGCAGGTG	GTGTGGCAGC	CAATAAAGGT	CTCAGAGAAC	GCCTAGCAGC	CGAGGTTACA	300
GATGTCAAGG	TCATCATTC	ACCTCTGCGC	CTCTGCGGAG	ACAATGCAGG	TATGATTGCT	360
TATGCCAGTG	TCAGCGAGTG	GAACAAAGAA	AACTTTGCAA	ACTTGGACCT	CAATGCCAAA	420
CCAAGCCTCG	CTTTTGATAC	CATGGAATAA	AGAGTGGCTC	TTTGTCAAGT	GTAGTGGGTA	480
GGCGAAAAGC	TACAATCTGG	AGANTACGAA	ATTC			514

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

CTTGGATTAT	AAAATACAAT	CGGCAAGATC	ATAAGTCCCA	AGCCTAAAAA	TATATAGAAA	60
GGGGGTCACC	TTCCAAAGAA	ATTCTGTATT	AAAGAGCATG	ACCACAAAAC	CAATCACAAG	120
CCCCAAGGCA	ATCCAGGCGA	CCTGCTGCCC	TAAAATGGGC	AGAATATTAT	TGGGGTAATC	180
ATGACTAACG	GCTATATAGA	TAGCCACCAC	ACCGATGACC	AGTAGAAAAA	ATACTGGCAA	240
GAGCAAACG	TAATCGACTC	TTGAGTCGAG	AGAACGTTTC	ATATAAACTA	ACCTTATACT	300
TTCATACAAT	ACTATTTATC	AAAGTTCATT	AAAAAATCTA	TCAATAGCCT	CGTCAACTTC	360
GGATCGAGAG	ATGGTTTAA	CAGTCGCTTC	TTCTGCTAGA	GATGCTACTA	TTTGTGTTGCC	420
GTATCGTTTT	CCGACGATTC	TCCTATCCAA	AATAAGAGTT	AAGGAACGTT	GGTATTCACG	480
TCTCATACTT	CTTCCCAAAG	CCTGTTTTAA	ACGAATAATG	G		521

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CTTGCCTGAT GACATCATTG ACTCTTTTGT GTATATCATC GACCATTCTT TAAAAAATGT	60
CTTTGAATTG GAAGAAGAAC TCGAGTTTCA ATTGCTTAAT AACCAAGGAA AGATTACCTT	120
CCACTTTTCA AGTCAACACC TCCCTACAGC CATTGATTTT GACTTTAACC ATCCTTTCGA	180
CCCTCGTTAT CCCCCAAGAG TACTGGTTTT AGACATGGAC GGTAGAGAAA CTATCCTCCT	240
CCCAGAAGAA AATGACCTAT TTTAAAAACT CTAGCCTTCA GTTGCAAGTG ACTGAAAACT	300
AGAGTTTTTC TATTTTTTCA AAGCATCATA CAAGTTGCGG ATCGGTTGTT TTAATATCGG	360
ATGGATAAAA TGAGGCGCAA TTTCTGTAA GGAACAAGG AAAAAAGGC GTTCCCGCTA	420
TGTTAAGGGA TGAGGCAATA TGAGGTCGTC TGTATAAAGG ATCTGGTCCT CCCACAAAGA	480
GCAAGTCCCA AATCAATCCA AACGAAGTCC CCCAATGCAC TTCTCTCACC CGTCCCCAGC	540
TCTTGACTCC AATGGCTAAC AAGGTTTCNT AACAATTCTT GTTGCTGGTA GCCAAGTTC	599

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CTATGGGTAA AAAGGATGCC TCTGCTATGC ATGAGATGAG GGCTTCCTTT ATTCAAGGCT	60
CCATAGAAGC AGGCCATACT GCGGAAAAAT CAGAGCAGGT TTTTGATGTT ATGGAGAAGT	120
TTGCAGGTTA TGGATTTAAT AGATCTCATG CCTACGCCTA CTCAGCCTTG GCCTTCCAGT	180
TGGCTTATTT CAAAACGCAT TATCCAGCCA TTTTTTATCA GGTCATGTTA AATTATTCCA	240
ACAGTGATTA CTTAATAGAT GCACTTGAAG CAGGTTTTGA AGTAGCCTCT CTATCCATCA	300
ATACTATTCC CTATCACGAT AAAATTGCCA ACAAGTCTAT CTATATAGGT TTGAAATCGA	360
TTAAGGGGCT CCAGCAAGGA CTTGGCGCTT TGGATTATTG AACATAGACC TTATTCTAAC	420
ATTGAAGATT TTATAGCTAA ATTACCTGAG AATTATCTGA AACTTCCTCC TGCTAGAACC	480
TTTGGTAAAA GTTGGTCTTT TCGATTCAAT TGAAAAAAT CGTCCAAAAG TATTTAATAA	540
CTTAGCTATC TATTGAATTG TGAA	564

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ACTAATCACT	TACTACGTAG	CTTCTGACTA	TCTACCTCTA	CTAGATAAAG	GACAAACTGT	60
AAGATTAAAA	CTGGAGAAGN	TTGGAAATCA	CGGCATTACC	ACCATCGGCC	AACTTCAGAC	120
AATTGATCAA	ACTCCTACCA	GAACAGAGCA	AGGCAATCTC	TTTAAATTAA	CCGCTCTTGC	180
AAAACATATCT	AATGAGGATA	GTAAACTCAT	CCAATATGGC	TTACAAGGTC	GCGTCACTAG	240
TGTAAGTGCA	AAGAAAACAT	ATTTTGATTA	TTTCAAAGAT	AAAATTTTAA	CCCATTCTGA	300
TTAATTTTCA	GATAACACTC	TATAACTATT	TATTATCTTA	TCAAAAAGGA	GAATCATAAC	360
ATGGATAAGA	AACAAAACCT	AACTTCATTT	CAAGAACTAA	CAACTACCGA	ACTCAACCAA	420
ATTACAGGTG	GAGAATGGTG	GGAAGAAGTC	TTACATGAAA	CAATTTTAAG	TAAATTTAAA	480
ATCACAAAAG	CACTTGAACT	ACCTATTCAG	CTATAAAAAC	AAGACCGAGA	AACAAGAACT	540
CTCGGTCTTG	TTTTTTATCA	TTCTGCATGT	ATCACAGTAA	GTACCTGACG	AAAGACTTGA	600
TTTTGGCGAG	GTAGTATT					618

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CAGGGGATGC	CAGTTGATTT	GCTTCAAGTT	GACTTGACTC	GTACTTGGA	AATCCTCGGA	60
GAAATCACTG	GGGATGCTGC	TCCAGATGAA	CTCATCACC	AACTCTTTAG	CCAATTCTGT	120
TTAGGAAAAT	AAGAAAAATC	CATGATCCTT	CATTCGGTCA	TGGATTTTAT	TGTCTTTATT	180
AGTAATCTGG	TCTTAAGACC	CCTGTTACAG	TTGCCCTAGT	TGCTTCGTAG	TCGCCATCTA	240
CGACAACCTT	GATAATGCGT	TTGACATCTT	CTTCTGGTGC	TGGAACAAGA	GGTAGACGAG	300
TGGGTCCAGC	TTCAAATCCC	ATATAGTTAA	GAATTGCCTT	AACTGGAGCA	GGACTTGAT	360
AAGAGAAGAG	AGCATTAACC	TTAGGAATGA	ATTTACGCTG	AATTGCTGCG	GCTTCTTCA	420
TATCGCTTTC	TGCAATGGCA	GTAAACATCT	CGTGATTTTC	ATCCCCATTT	GTATGAGAAG	480
CAACAGAAAT	AACCCATCCG	CCCCAAGGTT	CATGGCATGG	AAAGCATCTC	CATCCTCACC	540
TGTATAAAT						549

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

CTGGCTANCA AAATCATACT CATAATCCTT AACACCGACA GAGATAGAAG CAATGAGCCC	60
TTGATCGTGC ATTCGTTTAA TAAAAGGAAT GCGTCCTGCC TCATCAAAAC GGTGCATAAG	120
TGTACAAGTA ACCACCTTTA GCCAGTTGCT CTGCTACATT TTCATCCAAA ATCGTCTGCA	180
TATTCGCTGG CACAACAGGT AGTTTAAAGG TGTGATTTC TAAAGTGACA CTTGTATCCG	240
CTTCTGCACG GCTTTTAATG ACACATTTAT TTGGAATCAA TTGAATATCT TCGTAATCAA	300
AAATTGGAAA TTCATTTAAC ATATCGATGT CTCGTTTCTT TTGTAATGAC CTACCTATGC	360
TCTCGCATCA CTACGCCTTT TCCGACGTTT CCCTTAAATT TATTATAAAC CAAAAGTACA	420
GTTTTTGTC AATTATTTCA TGAATNAAAT ATATC	455

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 776 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CTCCTGGGTT TTGATTAACT CTAGGGTTGC CAAAAAGAGG GTGATGACTT CTTGGACATT	60
CTGGGCTTCC TTGAACAAAT CCTGCAAGCG CAATTGATTT CGTCCAATCA AGGATTCTTT	120
CACAATAATC ATCATGTCCT CAATCTTATA CTCATCCCGC AAGATAGTCG TGTGATTTTG	180
TGCAAACTCC TCTTTTTTCT TGGCTAGGAT ATTTGAAAAA GCCAAAAAGA GGTCAATGGT	240
CGTCTTGTC TGCACAAGCT CCGCATCTTC GTAAATCAAC TCTATCGGCG CTTTGGGAATA	300
ATACTGGGCC CGTTTCTTGG TGCTTGGCTT CCAAGTGCTC ACCCAAGAGC TTGAACTTGC	360
GATATTCTTC GATTTGAGAG AGGAGGTCCT GCTCCAGGTC ATCCCCCAAG TCTGTCACTT	420
CTGCTACCTT CGGAAGGAGT TTACGACTCT TAATCAGCAT GAGCTGACTA GCCATGACCA	480
TGTACTCACC CGTCACTTCC AGACGCATGG CCTGCAGGGT TGAGACATAG GCTAGATACT	540
GTTCGATGAC TTCCGTAATG GGCACATCGT AGATATCCAT CTGGTACTTA GAAACCAGAT	600
GCAAGAGTAA GTCCAGGGGT CCTTCAAAAT CTTTAAATTT AATATCCATT ATCTATATTT	660
TTCTAAGGTC AGGACTGTTT TTAATCCTAA TTTTTTTGCA ATTCGTACA AATCGACCTT	720
GTTTTCTATT TGTCCCTAGA ATAACTGTT CACGTAAGAC TTGAGATCGA ATTCCT	776

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

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ATTGATACCN ATTGTACAGG ACAACTTATT TTGGAGCGCC ATAGCAGGGA TANGGTTAGC      60
AATAGATGCG NTGACCATAG AAACGTTTNT TAGCCAATAC ATAACCTGCT AGAGATGAGG      120
TTGCACAAAC TAAGAACATG GTTACCAATG AGATAAAATAC TGAGTTCCAC ATCCATTGCA      180
AGGCAGGGTT CTGCACCATG AGTTGTTGGA AGTTTTCAT GGTGTCATT TTAGGGAACC      240
ACTGAGGAGG AATAACAATT GTATCAGGTT GTGATTTGAA TGCCCCTGTC AAAATCCAGT      300
AGAATGGAAA GATGNACAGC ACAGTCAACA AGAGCAAAAT GATTGTTGAA ATNACAGTAA      360
AGGCTGTAA TGGTTTTTTT TCTGTAGATT GCATAGCTGT CTCCTTTCTT TAGTATTCTA      420
CGTCGTTTCC AAGTACTTTA AATTGAACAA AGCTTACGAT AGCAATCATG ACTGCCAAGA      480
AGACACCAAT TGTGTTGGCA TAGCCGTATT CTGTCAATTG GAAGGCTTTT TCGTAAAGGT      540
AGTACATCAA GGTACTTGTT GAGTAGTTTG GACCACCAGA TGTCAAAGC TGAATCAAGG      600
CGAAACACTG GAATGAGTTA ATTGTTGTGA TGATTGCAAT ATAAAGAGTT GTTGAAGAA      660
GGCTTGGCCA TTTAATCTTC CAAAAACTT GAAACTCAGT TGCACCATCA ACACG      715

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(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

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CTGGGCTGAG TTTTCCAGAT ACAAATACTG CAACCGCAAC TGCAATCCCC CAACCCATAG      60
TAATCACAAT CCAACCTGCA CTGTTGCTCT TGGTTTTTGG AAGAACCACA CCTGCAACAA      120
CACCATTTC TAGAAGAATC AGGATTAAAG TCCCTAAAAA TTCTCCAAAT AATTCACTCA      180
TCATTTTTCT GTCTCCATTA AAAAGAAGGG GCGGGCGACA AGGATTGCTA CCCTCCACCT      240
CTTTTATTTT TTCTTAATTT TTTAATTCTG CTAAGTCGTT TTGAGCAAGA GCTGCTTTTA      300
CATCAGCACG GTAAGTTGCT TTTTCTTCTT CTGTCCAGTC ATAGAATCGT CCCATTTTCA      360
CCAAAACCTG CTCAACGATA CTATCCAAGC TATCACGCAT AAAGAGCATG TGATTGGTAC      420
GACGAAGAAG GAAGTCAACT GGGCTAAGAG TCAACTCATT GCGCATTGCA TAGTGAAGGG      480

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(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

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CTTAATTATA ACTTAAACAC AAAAGTTTTA CACAAACTGT GGATAACTCT TTTGAAACTG      60
TGATTTTCTT AATTGAAATC TATTTTTTAT TTTGTGAATA AGATGTGAAA AAATAGAGAA      120
TATGTTAGAA TAGAGTCATG AAAATTAAAG TTGTAACAGT TGGGAAACTG AAAGAAAAGT      180
ATTTAAAAGA TGGTATCGCA GAGTATTCAA AACGAATTTT TAGATTTGCT AAGTTTGAAA      240
TGATTGAGTT ATCAGATGAA AAAACACCAG ATAAGGCCAG TGAATCAGAA AATCAAAAGA      300
TTTTAGAAAT AGAAGGTCAG AGAATTTTAT CAAAAATTGC TGACCGTGAT TTCGTTATTG      360
TGTTAGCCAT TGAAGGGAAA ACTTTCTTCT CAGAAGAATT TAGTAAGCAG TTAGAAGAAA      420
CTTCTATAAA AGGANTTTCT ACTCTTACTT TTATTATTGG GGGAAGTTTA GGATTGTCAT      480
CATCTGTAAA AAATAGAGCC AATCTTTCTG TCAGTTTGGG TCGCCTAACC TTGCCTCATC      540
AGTTAATGAG ACTAGTTCTT GTTGAACAAA TCTATCGCGC TTTTACGATT CAGCAGGGAT      600
TCCCCTACCA TAAATAGAGA ATTGACTTTT AATTGAATTT TTGGTAGAAT AATTGTGTTA      660
GGTCTCATAG                                     670

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(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

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CTATAATTTT ATTAGCTGTA TTCCAGTCGT CACGACCAAA CTCTGTTACA GGGACACGAA      60
TGTCAAAACG GTTCTCAATC TCCACAATCA ACTCAACCGT TCCCATACTA TCCAAGACAC      120
CTGCATCAAA AAGATCTTCA TCCATCATGT CAGAAACATC TTCCATAAAC AACTCATCAA      180
TAATTTGAT AACTTCTGAT TTGATATCCA TATTTTATTT CCTTTTATTT TTAAACCAT      240
AGATTATTCA AGAATCCAGA AAAGATTAAG AATGACAACA TGACAACATG GAAAGTGACA      300

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ACCATGCCAA	GCAACTGAAT	CCAGCGATTC	TCAGGTAGGG	CAGCCTTCCC	TGCTTTTTTTC	360
CGTTCCTTAT	TGAGCGTTTT	TTTCTTGCGA	ACCCAGGCAT	CATTGATGAA	CAAGCCTAAG	420
TCCATGAAAG	AGTCCCATAG	GCGATATAGT	ACCAGGTCAC	ACCATGCCAA	AATCCCCATA	480
ATCCAGCATA	TTACAATGT	AAGATC				506

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ATGGTTCGAC	CCACAAATAT	GTTTTGCGAA	TCATTGACCA	TTCTATGATT	TACGTTGCCA	60
TTGCCGGCTC	ATACACGCCC	GTTGTCTTGA	CCTTGATGAA	TAAGTGGTTT	GGCTATCTGA	120
TTATTGTCAT	CCAATGGGGA	ACGACCATCT	TTGGTATTCT	CTATAAAATC	TTTGCTAAAA	180
AGGTCAATGA	GAAATTTAGC	CTTGCTCTTT	ACCTGATTAT	GGGCTGGTTG	GTTCTGGCTA	240
TCATTCTGTC	CATTATCAGT	CAAACNACAC	CCGTTTTCTG	GATTCTCATG	GTAAGTGGCG	300
GACTCTGTTA	TACAGTTGGA	GCTGATTGAT	AGCCTTTATG	CATTGAAATT	TGACAGTTTG	360
ACTTATGAAA	ATAAAGCAGA	GGTTATGGAC	TTTATCAAGG	CTCGTGTTGA	TAAGATGATG	420
GGCTCTACTC	CAAAAGATAT	CAAGGGAAGC	AGTTCTTGCA	GGTTCAAAC	TTGTTGTGGC	480
AGATATGTTT	GGAAGCAGCA	AGTGCTCTCG	TAGAAGTAAG	CAAGGAAGAA	GATTTTAAAC	540
CATCTGTTGA	ATCACTTTCT	CGTGCCTTTA	ACCTGGCTGA	GAAGGCAGAA	GGGGTTGCTA	600
CAGTTGATTC	AGCACTATTT	GAGAATGACC	AAGAAAAAGC	TTTGGCAGAA	GCAGTAGAAA	660
CACTCGTTTT	ATCAGGACCT	GCAAGTCAGC	AATTGAAACA	ACTCTTTGCG	CTTAGCCCAG	720
TCATTGATGC	TTTCTTTGAA	AATACTATGG	TAATGGCTGA	AGATCAGGCT	GTCCGTCAAA	780
ATCGTTTGGC	AATCTTGTCA	CAACTAACCA	AGAAAGCAGC	TAAGTTTGCT	TGTTTTAACC	840
AAATTAACAC	TAAATAAAAT	TTGATAAACG	GACTTTATCT	TATTACAAAG	GAGAAGAAAT	900
GGATCCGAAN	ANATTGCTCG	T				921

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

CTTGGCAACA GGCTCTTTTT GTATTGCGTT TATTAAGAAA AACAAAAAAC ATCGATATAA	60
CATTTAACTA AAAATTATTG TATGTTATCT CCCTTAATTA GGAATGATAA GGAATAACT	120
AGAAAGATTT GTGAATACAA ACTATTTCTG ATATACAAAA TATACAGTAA TAATGAATGA	180
TGGGAGATGG GATGAAAGAA TTTCAATTTG AGAGAAAGCA GCGTTTTTCT TTGAGGCCAT	240
ATGCAATAGG AGCTTGTTCTG GTCTTGCTAG GAACGAGTTT ATTTTTTGCT GGTATGGGTG	300
CTCAGCCTGT ACAGGATACA GAAACGAGTT CAGCACTAAT TTCAAGTCAT TATTTGGATG	360
AGCAGGATTT ATCTGAAAAG CTGAAATCTG AGTTGCAATG GTTTGAATTA GAAAACAAGC	420
TTTTGAACTT ATGGGAACAT TAGGTTACTA TGAAGGATTT GTTCCTTATG TTTCAAATCA	480
ATACAAAAAC CAAGCTGAAG AAGAAGGCAA ACCGCTATCT GATAAATATA TTTTCGAAAA	540
ATCTTAAGAA AAACATATGC ACCTTCAAAA A	571

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 611 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GTATCAACTC CAAAGAGCAA GTGACTGTCA AAGTTGTAAC AGATGCGGCC AAGAAGCTCA	60
TGGGTGATAA GATTGCTCGC CAGAAAGAAC GTGGGATTCA GATTGANACC TTGCGNACCA	120
TGATTATNGG GATTCCANAC GNTGGTAAAT CCACTCTGAT GAACCGTTTG GCTGGTAAAA	180
AGATTGCTGT TGTGGAAC AAGCCAGGGG TCACAAAAGG TCAACAATGG CTAAAACCA	240
ATAAAGATCT GGAAATACTT GGATACACCG GGGATTCTCT GGCCTATAGT TTGAGGATGA	300
AACTGTTGCA CTTAAGTTGG CATTGACTGG AGCTATCAAG GATCAGTTGC TTCCTATGGA	360
TGAGGTTACC ATTTTGGTA TCAATTATTT CAAAGAACAT TATCCAGAAA AGCTGGCTGA	420
ACGCTTCAAA CAAATGAAAA TTGAAGAAGA AGCGCCTGTG ATTATTATGG ATATGACCCG	480
CGCCCTCGGT TTCCGTGATG ACTATGACCG TTTTACAGT CTCTCCGTG AAGGAAGTCC	540
GTGATGGCAG ACTCGGTAAC TATACCTTAG ATACATTGGA AGACCTCGAT GGCNACGATT	600
GACTAAGTC C	611

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1054 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

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TTGCTAAAGC AGCCATGATG ANGGCACTCC ATAAGGATAA GTACCACCAA GCAGCAGCAG      60
ANGACCATAA TCTCCTTTAT GACTTGAACG AGAACGTTCA ATAATAACTT TTTCTAGTAA      120
GGTTTGATTA ATCACTTTCA TCCTTTTTCCT CTCTCACTTT TATTATACAA CAAAAAGGAG      180
ACGCAGACCT CCTTTTGTA TCTTATATCT AAAATTTAAT ATTCATTTCT GCCATTTTAG      240
ATATAGCTAT AGAAAATACA CTCTATTAAT CGAATGTTTC TCTTATTTTC TATCCAATGT      300
CCGAAGTGCT GCTTGATAAG TTTGCTCCAT CAGCATGGTA ATGGTCATAG GACCGACACC      360
TCCAGGGACT GGC GTGATAT GGCTAGCAAG TGGTGCAACT GCCTCATAAT CAACATCTCC      420
ACAGAGCTTC CCATTTTCAT CTCGGTTCAT CCCAACGTCA ATGACAACCG CACCTGGTTT      480
GACAAAGTCA GCAGTCACAA ACTTGGCGCG GCCGATTGCG ACTACAAGAA TATCTGCTTT      540
AGCAGCCACC TTGGCAAGAT TATGAGTTCG TGAGTGGGCC AAGGTTACTG TCGCATTTTT      600
AGCCAAAAGA AGCTGAGCCA TAGGTTTTC AACGATATTT GAACGACCGA TTACGACCGC      660
ATTTTTACCT TCCAAGTCAA TCCCATATTC ATGAAACATT TCCATAATTC CTGCAGGTGT      720
CGAGGGAATC ATGACTGGAT GTCCAGACCA AAGACGTCCC ATGTTTAGGG GATGGAAACC      780
ATCCACATCC TTTTCTGGGT CAATGGCTAA TAAAACCGCC TCTTCATCGA TATGTTTGG      840
TAATGGCAAC TGGACCAAAA TCCCATGCCA AGCTGGATCC CTGATTATAT TTAGCAATCA      900
GGTCTAACAA TTCCTCTTGA GTTAATGGTC TCTGGAAGTC GCACTACTTC GCTACGGGAA      960
CCAGCCGCAA GAGCTGACCT CTCCTTGTTG CGAACGTAA ACTTGCTGG CTGGATTATC     1020
CCCAACCAAA ATCACTACCA ACCAGGCACT AGAG                                1054

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(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

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CTGAACTGGA TTTTGCTACA AGGTCTGATT TGTCAAAGAG ATGCGAGTTA TGATATGAAG      60
CAGGATGATT TGGATAAGGT AGCAGATTAT CTCTTCAAAA CAGAAGAATG GACCATGTAT      120
GAGTTGATTC TTTTCGGTAA CCTCTATAGT TTCTACGATG TAGACTATGT CACTCGGATT      180
GGTAGAGAAG TTATGGAGAG GGAGGAATTT TACCAAGAGA TTAGTCGCCA TAAGAGATTA      240
GTGTTGATTT TGGCCCTCAA TTGTTACCAG CATTGTTTAG AGCATTCCTC TTTTATAAT      300
GCCAACTATT TTGAGGCTTA TACAGAGAAG ATTATTGACA AAGGTATTAA GCTTTATGAG      360
CGTAATGTTT TCCATTATTT AAAAGGTTTT GCCTTATATC AAAAAGGACA GTGTAAAGAA      420
GGCTGTAAGC AGATGCAAGA GACCATGCAT ATTTTGTATG TGTAGGTCT TCCAGAGCAA      480

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GTTAGCCTAT TATCAGGAAC ACTACGAAAA ATTTGTCAAA AGTTAATTTT CCCAAATAAG 540
GGAAAAAATA AAAAGCTCCT TTCGGTTTTG ATACAATAGT TTCAAATTT GAGAGGAG 598

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

CTACTTCCCG GCCGAGTCGA TTCTCCGCCG ATATCGAGCA TACTGGCTCC TTCTGTTATC	60
AATTTACGAG CCTGCTGGAG CGCCTGCTCA AGAGCAAAAA ATTGACCACC GTCCGAAAAG	120
GAGTCTGGGG TTACATTGAT AATTCGCAA ATAGCTGTCT TTGCATGAGT GGCTTTACTG	180
GACATATCGG TCACTCCCTC AAGGCTATTC ATCATATTAT TTCTCTATTT TACCATAAAA	240
AGAAAAAGAT GGACACGATT TCATTCATCT TTCTCCCAGT AGAAACAAGT AAGCAATTGT	300
CAATAATCTT AAACAGAAAT CCCTAATGTC CGACTCATAA TCACCACAAG AGCCAACAAA	360
CAGAAAGCAA TCCCATTAAC AATCATGTGA AGTAAGATCG ACATTTCCAA ACGTTGGGTC	420
TTGTAGGCTG TCCAAGATAG AACTGTGCGAC ATACCTCCAT AAATCAATAA AGAAGGTAAA	480
TTACTTGGTT GATGTAATAA AGCAAACACA ATCGTACCGA CTACAAAT	528

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

CTATGAGAGA GAATGACCTT CTCTTGATTA CTGCGGACCA TGGAAATGAC CCAACGTATG	60
CAGGAACGGA TCACACTCGG GAATATATTC CATTGTTGGC CTATAGCCCT GCCTTTAAAG	120
GAAATGGTCT CATTCCAGTA GGACATTTTG CAGATATTTT AGCGACTGTT GCCGATAACT	180
TTGGTGTGGA AACTGCTATG ATTGGGGAAA GTTTCTTAGA TAAATTGGTA TAAGATGACG	240
CGCTATGCTT TGCTGGTGAG AGGTATCAAT GTTGGTGGTA AGAATAAGGT CGTCATGGCG	300
GAGCTTCGTC AAGAATTGAC AAACCTGGGA CTGGAAAAAG GTTGAGAGCT ACATCAATAG	360
TGGCAATATT TTCCTTTACT TCGATAGATT CCAAAGCCCC AATTGGTTGA AAAAGCTAGA	420

GACTTTCTTT GCAGTCCATT ATCCATTTAT TCCAGAACTT TTTCCTTTAC TGAGTCTAGA 480
GGACTTTGAA GGGCGGAACT TGAAA 505

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

CTATTTCTC	ATCTTTT	TA GACTGGTAAT	GTATCCCCTA	GAGTTTCATT	GTTAAGACCT	60
GTCGTATTGA	CAACAGTGA	TCCTGATTCC	CCATTCCAAG	AGTTTGGCC	GCATCATATN	120
GACGAAATCT	TTTTCTGAGC	CAGCAATTTT	CTCAGCTAGG	GCAATAGCGG	CGCTGTTGGC	180
ACTAGATACC	AGAGTTGCTT	CAAGCAACTC	TTCGACAGTA	TAATTACGGG	CCTCCATAGG	240
AATATTACTG	GCTTCAGAAT	TTGTCGTCAA	TTGATAAGGA	TAATCAGAAA	TATCTACAGG	300
AGTGGAGAGG	GTAATACTTC	CGTTTTCCAA	AGCTTCATAG	ACCAGATAAA	CAGTAATCAA	360
TTTTGTATG	GAAGCAATTT	CGACAGGTGG	CGTTGCATCC	TTCTCATAGA	GAATTTTACC	420
AGTATTTGCC	TCAACAGCAA	TCGCATGTTT	AGCGGCAATG	GTAAAATCTT	GAGCAACAGC	480
AGTAGAAGCA	CCCCCTAAAA	GAGAGACAGT	TAACAAAGTT	AAAAATATTT	TTTTCATAGT	540
AGTCTTATTC	TATCATAAAG	AAAAAAAAATA	TTCTTGCTTT	AATAATTCAT	CTGTTAAGCT	600
TTTTGAAAAT	ATGGTAAAT	AAAGTGAGGG	AGGTAACTCA	TGTTTCGTAG	AAATAAATTA	660
TTTTTTTGGG	CCACAGAAAT	TTTACTCTTA	ACCATCATCT	TTTACCTATG	GAGACAGATG	720
GGGTCTTTGA	TTAACCCTTT	TGTTAGCGTG	CTTAATACAA	TTATGATTCC	ATTTTTATTA	780
GGGGGCTTTC	TTTATTATTT	GACAAACCCT	ATTGTTACTT	TCTTAAATAA	AGTCTGTAAA	840
CTCAATCGTT	TGCTTGGTAT	TTTAATTACC	TTGTGT			876

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

CTTGTCAAAT GCCATGGAAG GGGTTCTTTA CTCCTCAAA CCAGACTTTT CAAAACCTGAC 60

TAGCGCTGAT	CTCCTCTATG	CTCTGGGACA	ATCTTTCTTT	GCCCTCTCAC	TAGGGGTTAC	120
AGACATGTTG	ACCTATGCTT	CTTACTTGGA	CAAGAAAACC	AATCTAGTCC	AGTCAGGAAT	180
CTCCATCGTA	ACCATGAATA	TCTCGATAGT	CCATCATGGA	AGGTCTAGCC	ATTTTCCCAG	240
CCATGTCAGC	CTTCAATATC	CACTCTGAAA	GGGGACCCAG	CCTGCTCTTT	ATCGTCTTGC	300
CTCAACTCTT	TGACAAGATG	CCTTTTGGAA	CCATTGCTA	CGTCCTCTTC	CTCTTTGCAA	360
CTGTCACTTC	TTCTGTCGGT	GATGCTGGAG	ATCAATGTGG	GCAATGTCAC	CAACCAGGAT	420
AACAGCAAAC	GTGCCAAATG	GAGTGTTATT	TTAGGAATTT	TGACCTTTGT	CTTTGGCATT	480
CCTTCAGCCC	TATCTTACGG	TGTCATGGCG	GATGTTTACA	T		521

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 553 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

CTGCAGACAA	TAACTTGGTT	AGCTTAACGG	CTCTTGAGGA	TTCATCCAAG	GATGTAACCT	60
TTACCAGTTC	GGCTTTCAAT	CTAAAAGAAG	GGCGACACCT	TCAAAAAGGG	GATTCCAAGA	120
AAATCCTTAT	CCACGAAGAA	TTGGCTAAGA	AGAACGGTCT	TTCACTTCAT	GACAAGATTG	180
GCTTGATGTC	TGGTCAGTCT	GAATCTGGAA	AAGGACAAAC	AGTAGAGTTT	GAGATTATCG	240
GCATCTTTCC	TGGTAAAAAA	CAAGAGAAAT	TCACAGGCTT	GTCTTCTGAC	TTCAGTGAAA	300
ATCAAGTCTT	TACAGATTAT	GAAAGTAGCC	AAACCCTTTT	GGGCAATAGT	GAAGCTCAAG	360
TCAGTGCAGC	ACGCTTCTAT	GTTAGAAAAT	CCTAAGGAAA	TGGACGGACT	CATGAAGCAG	420
GTAGAAAACT	TGGCCTTGGA	AAATCAAGGC	TACCAAGTCG	AAAAGGAAAA	CAAGGCTTTT	480
GAACAAATCA	AAGACTCAGT	TGCAACTTTC	CAAACCTTCC	TGACCATCTT	CCTTTATGGA	540
TGTTGATAGC	AGA					553

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 523 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

CTATGGATGC	GGAAGTTTCT	AAGAACCCTC	GCTTGATCCT	TGAGCGTAAA	GGAATGACCA	60
TCTTGACTGG	TACTAAACTG	CAAGAAATCA	TTGAGGAAAA	TGGTCAACTT	CGTATCAAGG	120
TTGAAGGAAA	AGACAATATC	ATCGCAAGCA	AAGCTCTTCT	TTCAATTGGT	CGTATGCCAG	180
ACCTTGAAGG	TATTGGAGAG	GTTGAGTTTG	AATTGGATCG	TGGTTGTATC	AAGGTCAATG	240
AATACATGGA	AACTTCAGTT	CCACGCATTT	ATGCCACCAG	GTGACATCAA	CGGTACTAAG	300
ATGTTGGCTC	ACGCAGCTTT	CCGCATGGGT	GAAGTTTCCG	CTGAAAATGC	CCTTAAAGGA	360
AATCATGCAG	TTGCCAAATT	GAATTTGACT	CCTGCAGCCA	TCTACACTCT	CCCTGAAGTA	420
GCAGCAGTAG	GTTTGACAGA	AGAACAAGCC	CGTGAGAAAT	ACGATGTTGC	CATCGGTAAG	480
TTTAACTTTG	CTGCTAACGG	TCGTGCTATT	GCATCTGACG	CAG		523

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

CTGCAGGTGG	AATTATGAAT	GTCGGATATG	AAAAAGCATT	CTTGATGCAG	ACATCGTTAA	60
ATTTGCCAAC	TTCTGAAATT	ATCTCGACAT	ATGTCTATAA	AGTTGGTCTT	GTATCAGGAG	120
ACTATTCTTA	CTCAACAGCG	GTTGGTTTGT	TTAATGCAGT	GATTAACGTA	GTATTGCTTG	180
TTGCAGTTAA	CCAAATCGTT	AAACGCATGA	ATAATGGTGA	AGGAATTTAA	GGAGGAAAAGT	240
ATGAAAAATT	CGATTATGGA	TACAAAATTT	GATAGACGTA	TCTTACTCTT	AAATAAAATC	300
ATTATTGTCT	TTATCGTTT	GATGACTTTG	CTTCCTTTAC	TTTATATCGT	CGTAGCATCC	360
TTTATGGATC	CTAAGGTTCT	GGTTAGTAGA	GGGATTAGCT	TTAATCCAGC	CGATTGGACT	420
GTAGAAGGTT	ACCAGCGTGT	TATTCAGTGA	CCAATCTATT	CTAAGAAGTT	TTATCAATTC	480
CCTACTATAC	TCTTTTGGAT	TTGCAGCT				508

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CTAAAAAGAA	CCAGATGGAT	CTTGTGATGA	ATTTACATCA	TTTTGATTTA	CCAGTGGAAC	60
TTCTTCAAAA	ATACGGTGGT	TGGGAAAGCA	AACATGTAGT	GGAGTTATTC	GTGAAGTTTG	120
CCAAGACTGC	TTTCAACATG	CTTTGGAGAT	AAGGTTTCATT	ACTGGACAAC	TTTCAATGAG	180
CCAATGGTCA	TTCCAGAAGC	AGGATACTTA	TATGCTTTCC	ATTATCCAAA	TCTAAAAGGA	240
AAGGGAAAAG	AGGCCGTACA	AGTCATCTAT	AATCTAAACC	TTGCTAGTGC	AAAAGTGATT	300
CAACTATATC	GCTCATTAGG	ACTTGATGGA	AAGATTGGGA	TTATTTTAAA	CTTGACACCT	360
GCTTATCCAA	GAAGTAATTC	TCCAGAAGAC	TTAGAAGCAA	GTCGATTTAC	AGATGACTTC	420
TTTAACAAAG	TCTTCCTTGA	ATCCAGCTGT	TAAAGGAACT	TTCCCAGAAA	AGATTGGTAA	480
AAACAGCTAG	AGAGAGATGG	CGTGTTATGG	AGTCATACCG	AAAAAGAG		528

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

ACTCTTATTG	GTGAGGTATC	GCAACTTCTG	TTTCTGCCTT	CCTTGGTGGA	CCAGCCAATA	60
CAACTTACGG	AGAAAATACA	GGGGTTATCG	GTATGACTCG	TATCGCTTCT	GTCTCAGTTA	120
TCCGTAACGC	TGCCTTCATC	GCGATTGCCC	TCAGCTTCCT	TGGTAAATTC	ACTGCCTTGA	180
TTTCAACTAT	TCCAAACGCT	GTA CT TGGTG	GTATGTCAAT	CCTTCTCTAT	GGGGTTATCG	240
CCAGCAATGG	TTTGAAAGTC	TTGATTAAAG	AACGTGTGGA	TTTCGCTCAA	ATGCGAAACC	300
TCATCATCGC	AAGTGCTATG	TTGGTTCCTG	GACTTGGGAG	GAGCTATCCT	TAAACTTGGT	360
CCAGTTACAC	TTTCAGGTAC	TGCCCTTTCA	GCCATGACAG	GAATCATCTT	GAAGTTGATC	420
TTGCCATACG	AAAATAAAGA	CTAAGAGTCT	AAATACACCT	AATCCACTCA	GACAGCTGAG	480
TGGATTTTTC	GTATACCATA	ATAAAAAGTG	CTTAACAAAA	TTATTAAAAT	CAAAAAACGT	540
ATAATATCAG	ATATTCTAAA	ACCTTGATAC	TGTACGTTTT	ATCATAGAAA	TTTTTACTTT	600
ATTTTCTCAT	CAAATGAGAT	TTGCATCAAT	CTCTTGCTCT	ACTTGCGTTT	CTTCTTCGCT	660
TTCTTCATTT	TGTTAGCCAT	ACGTTTCATG	GACTGTTTCA	TGGCAAATTC	ACCAATTTTA	720
CCTTTCAAAC	CGCCACCAAA	CATCTGGCTC	ATATCTGGCA	TTCCTGCTCC	TCCGAGAG	778

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

GGGAGTTGGT	TGCTATTNGT	GAGGGAAAAG	GTTTGAACTT	TGAAATCGAA	GTGGATGGTG	60
GGATTGATGA	CCAAACTATT	GCTCAAGCCA	AAGAAGCTGG	TGCGACTGTT	TTTGTAGCAG	120
GTTCCCTATGT	CTTTAAGGGA	GAAGTCAATG	AGCGAGTACA	AACTCTCAGA	AAACAACCTGG	180
ACTAGGGTTG	CAGTTTTTGC	AGGCGGAAAC	CGCGGTCATT	ATCGGACAGA	TTTTGATGCT	240
TTTGTGGGG	TGGATCGAGG	CTCGCTCTGG	GTCTTGGAAG	AAGACTTACC	TCTTGCTCTA	300
GCAGTCGGAG	ATTTTGATTC	TGTGACGGAA	GAAGAGCGAC	AGGTGATTCA	AAAACGTGCC	360
CAGTATTTTG	TCCAAGCCCG	GCCAGAAAAA	GATGATACTG	ATTTGGAATT	GGCTCTCTTA	420
ACCATCTTTG	AACAAAATCC	TCAGGCTGAG	GTCACTATTT	TCGGTGCCCT	GGGTGGCCGT	480
ATTGACCATA	TGTTGGCCAA	TGTTCTTTCT	ACCTAGCAAT	CCCTAAGTTG	GCACCCTATA	540
TGCGTTCNAA	TAGAAATTGA	GGAATGGGCA	AATTTGATTG	CCTATTGTTC	CAGAAGGGAA	600
CAGTCAGATT	CGAATCCCTG	CA				622

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

CTATTATCAG	CACTTTTATA	CCTATTACCA	AAAAAATCCT	CAAAATGATT	GGCAAAAGGC	60
TTTATCCACC	AGCCATTTAT	CAGCAATATT	TACTTGAAAA	ATATGGTAGA	AATAGAAAGG	120
ATGGAGGAAT	CTAATGGTAT	TACAAAGAAA	TGAAATAAAT	GAAAAAGATA	CATGGGATCT	180
ATCAACGATC	TACCCAACCTG	ACCAGGCTTG	GGAAGAAGCC	TTAAAAGATT	TAACAGAACA	240
ATTGGAGACA	GTAGCCCACTG	ATGAAGGCCA	TCTCTTGGAT	AGTGCGGATA	ACCTACTAGT	300
AAATCACTGA	ATTTTCTCTT	GAAATGGAAC	GCCAGATGGA	GAAGCTTTAC	GTTTATGCTC	360
ATATGAAGAA	TGACCAGGAT	ACACGTGTAA	GCTAAGTATC	AAGAGTACTA	TGCCAAGGCC	420
ATGACACTCC	TACAGCCAGT	TAGACCAAGC	CTTTTCATTC	TATGATCCTG	AATTTATGGA	480
TATTAGCGAA	AAGCAGT					497

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

CTGTTATGGA	GTTGAAAGAA	GAATACCACC	CAGACGGTAA	AGGTTTTGAA	ATGATCTGTA	60
TCGGTGGGAT	GGGAGCTGAT	TTCTTTAAGG	CTCGCGGTAT	TCAACCACTT	TATGAATTAC	120
GTGGCTTGTC	AGACCAACCT	AGCTTTGATC	AAGTTCGTAA	GATTATTTCA	AAAAGTGTG	180
AAATGTACCA	AAATGAACTC	TTTGATGAGC	TTTATGTTTG	CTACAACCAC	CATGTCAATA	240
CGCTAACCAG	TCNAATGCGT	GTGGAACAAA	TGCTTCCGAT	TGTTGACTTG	GATCCAAATG	300
AAGCGGATGA	AGANTACAGC	TTGACTTTTG	AAATTGGGAA	ACCAGCCGAG	AAGAAATTCT	360
GGAGCAGTTG	TTGCCTCAGT	TTGCAGAAAG	TATGATTTAC	GGTGCCATTA	TCGATGCCAA	420
GACAGCTGAG	AATGCTGCGG	GTATGACAGC	CATGCAAACA	GCGACAGATA	ATGCTAAGAA	480
AGTCATCAAT	GATTTGACAA	TTCAGTATAA	CCGTGCCCAG	ACAGGCGGAT	ATTACACAAG	540
AAATTACCGA	AATCGTAGCA	GTGCCTAATG	CCTTAGAATA	GCTCTAGTCC	CAGCTCTCCT	600
CACTC						605

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

CTACACTTGA	GGGAAGTTTG	AAAATTCCAT	TTTTCTTAAA	GGGAATTGTG	AAACGCTATG	60
TATTTTCTTT	TTACAACCGG	ATGGAGCACT	TGGTTGTGGT	CAATCCTATG	TTTATTGAGG	120
ATTTGGTAGC	AGCTGGTATT	CCACGTGAAA	AAGTGACCTA	TATTCCTAAC	TTTGTCAACA	180
AGGGAAAAAT	GGCATCCTCT	ACCACAAGAA	GAGGTAGTCA	GACTGCGCAC	AGATCTTGGT	240
CTTAGTGACA	ATCAGTTTAT	CGTAGTAGGT	GCTGGGCAAG	TTCAGAAACG	TAAAGGGATT	300
GATGACTTTA	TCCGTCTGGC	TGAGGAATTG	CCTCAGATTA	CCTTTATCTG	GGCTGGTGGC	360
TTCTCTTTTG	GTGGTATGAC	AGATGGTTAT	GAACACTATA	AGAAAATTAT	GGAAAATCCC	420
CCTAAAAATT	TGATTTTTC	AGGCATTGTA	TCGCCAGAGC	GGATGCGCGA	AATTGTATGC	480
TCTAACGGAT	CTTTTCTTGT	TGCCTAATTA	CAATGAG			517

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

TGTTGCGCTC	CATATCCNAA	ACTTGCCCTG	CCACCATACC	CAGACTACCT	GAAGCAAGGG	60
ATAAGTTGGC	AATCGAGCCC	ACCTNGATCT	GACTTGCGCA	ATCTGCCTGC	GCAATCAAGG	120
CATATGGGTC	TAAGAATAAG	GATCTCCAGC	CAAAATGGCC	ATAGCTTCAC	CGAATTTCTN	180
GTGATTGGTT	AACCGCCCTC	TTCGATAATC	GTCATCATCC	ATAGCAGGAA	GGTCATCGTG	240
AATCAAGCTC	CCTGTATGAA	TCATCTCCAA	GGCAGTAGCT	ACCTGCGCGN	GAGCAGGTTT	300
GATGGTAACC	TGCAAGGCTT	CCAGAACTTC	TAACAAGAGA	AAAGGCCGAA	TACGCTTGCC	360
ACCAGCATGA	ATAGAATAGA	GAACAGACTC	CCGTAAACTA	GAGGCAAACT	GCTGGTCTCC	420
ATAAAATCTT	CCAAAGCCGA	CTCGACAAGA	GCTAATTTTT	CTTGCTTTTT	CATTCAAAAT	480
CACTTTCTGT	TCCGTCTTCT	TGCATGACCT	TGACCAAGGT	CTTTTCAGCC	TTGTCCAGCG	540
TAGCTTGGAG	CTCTTTTGAC	AAGACCATGC	CCTTTTGAAA	GGCAGTAATC	GCATCTTCCA	600
GAGCAATTTT	ACCATTTTCC	AAACTTTGGA	CAATGGTTTC	CAGTTCTGCT	AGATTTTCCT	660
CAAATTTCTT	TTGTTTTGAC	ATCTTTAACC	TCTAATTCTA	CTTGACCATC	TCCGATCAAA	720
AGCGTTACTT	GGTCTTTTTT	CTTCAAATC	TCAACCGAAT	CTACAACGGA	TCTTCTTTTT	780
TGACAATAGC	ATAACCAC					798

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 547 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

CCATGTTTGC	GGCAGTGACA	GCAGGTTATC	AGGCTGCCCT	AATGGTACCA	ACAGAAATCC	60
TCGCAGAGCA	ACACTTTGAG	AGTTTACAGA	ACCTTTTTTC	CAATTTGAAA	CTGGCTCTCT	120
TGACAGGTTT	CTTGAAAGCT	GCAGAAAAGA	GAGAAGTCTT	GGAGACCATT	GCCAAGGGTG	180
AGGCTGATTT	GATTATAGGA	ACTCACGCTC	TGATACAAGA	TGGGGTGGAG	TATGCTCGTC	240
TTGGTTTGAT	TATTATCGAT	GAGCAGCACC	GTTTTGGTGT	AGGGCAAAGG	CGTATTTTAC	300
GGGAAAAAGG	CGACAATCCA	GATGTCTCTA	TGATGACGGC	GACTCCCAT	CCACGGACGC	360
TTGCCATCAC	AGCCTTTGGA	GATATGGATG	TTTCCATTAT	CGACCAGATG	CCAGCAGGTC	420
GGAAGCCCTA	TTGTGACGCG	CTGGATCAAA	CATGAGCAAC	TACCTCAGGT	CTTGACTTGG	480
TTAGAGGGGG	AAATTCAAAA	AGGTTCCCAA	GTCTATGTCA	TCTCTCCTTT	GATTGAAGAA	540

TCAGAAG

547

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

CTCTTTTAAC	CGTTTTAGCG	GTGACACCGA	GGTATTTTTT	CAGGACCCAA	GACTTGTCGG	60
GCAACCGAAA	CTGGGAGTTC	GTCATCTCCA	ATATGCAGAC	CAGCAGCATC	AACCGCAAGA	120
CAAACATCCA	ACCGATCATC	GATTATCAAG	GGGACCTGAT	AGGCATCTGT	TATTTCTTG	180
ACTTGTTTTG	CCAGTTGATA	ATATTGATTG	GTTGTGAGAT	TTTTTTCTCG	CAATTGGACT	240
ATG GTAACCC	CTGAACGGCA	GGCCGTCTCA	ACTTTTGCAA	GAAAGCTTTC	CACGGAATCT	300
TGATAGCGAT	TGGTTACCAG	ATATAGTCTA	AGCGCTTCTC	TATTCATAAA	CCTCTCCTTT	360
GATGGTATCT	AGCCAATTTT	CATCTCTTCT	TAGGAGCGAA	AGCTGATTGA	GTACTTGGTA	420
ACGAAATTCT	TCCAATCCCA	TTCCTTGAAC	AACTATTTTC	TCAGCCAGCG	ATATTGAGAT	480
AAGAGACTGC	TAAGCAAGAA	CTTCAAAACC	AGTCTTTCCT	TGGCTGAGAA	AAACAG	536

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 854 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

CTGGAGTGAC	GATTGAGAAA	ATCTTTGCCC	TAGAAAATTA	TCGAAATCAG	TTAGCTGCTT	60
TTCCGCAAAC	TGTCTGGATT	TCAGAGGATA	TTTGTCTAGA	TTTGGCGGAT	TCTCAGACTC	120
CACAGGGAAT	TGTTGCCGTG	GTTCAAAAAG	AAGAAGTAGG	ACAAGCTGAT	TTGAGTCAGG	180
GCAAGTTCTT	GTTTTTGGA	GATGTGCAAG	ATCCTGGTAA	TGTAGGAACT	ATCATTCGAA	240
CTGCGGATGC	AGCAGGTTTT	ACAGGAGTGA	TTGTTTCAGA	TAAGTCGGCA	GACATCTACA	300
GTCTTCAAAA	CCCTACGTTT	CATGCAAGGT	AGTCATTTCC	ATCTGCCCAT	TTACCGGATG	360
ACTAGTCAAG	CGCTTCTTGA	CGAAACTAAA	AAGGTAGCTA	TCCCAGTGCT	AGCAACAACC	420
CAATCTAAAG	ATTCTGTTGA	TTACAGAGAA	CTGCCTTCTA	TAGAAAATTT	TGTACTAGTT	480

ATGGGAAATG AGGGTCAAGG AATTAGTCCC CTTATGGCTG AAAGTGCAGA CCAGTTGGTC	540
CATATTAGCA TGAAGGGGCA GGCCGAGAGT TTGAATGTTG CGGTGCAGC CCGTATTTTA	600
ATCTTCCATT TAAGCTAATT TTAACTTTTT TTGTTATAAT CAAGGAAAGA TGTTACACAGA	660
AAAGGAGAAA TGGATGAATC ACACATTAT ACATGACCGT GCAGGTCTCA ATCAATTTTA	720
CGCTAAGGTT TATGCCTTTG TTGGTCTGGG AATCGGACTA TCTGCTTTGG TATCAGGCCT	780
TATGTTGACG GTCTTTCAGT CTCAGTTGGT TTAACTTTTG ATGCAGGGGC GTCTCTGGTT	840
GACCATTGCT ACTT	854

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

CTGAAGAAAT CCTAAAAGAT TTGTATTACG GAGCCGCTAA GAAAATTCAA GAAGAAGCCT	60
CTCGCTGGGC AGGAGTTGTA AGAAATGACT AAAACAGCCT TTTTATTTGC TGGTCAAGGT	120
GCCCAGTATC TACGGATGGG ACGGGATTTC TATGATCAGT ATCCGATTGT CAAAGAAACG	180
ATTGATCGAG CGAGTCAGGT GCTCGGTTAT GATTTACGTT ATCTCATCGA TACGGAAGAA	240
GACAAACTCA ATCAGACCCG CTATACGCAA CCAGCCATTC TAGCGACTTC GGTGCTATC	300
TACCGTTTAT TGCAAGAAAA GGGCTATCAC CCTGATATGG TTGCTGGTTT GTCTCTTGGA	360
GAATACTCTG CCTTGGTGGC AAGCGGCGCC TTGGATTTTG AAGATGCCGT TGCCTTGGA	420
GCTAAGCGTG GAGCCTATAT GGAAGAAGCG GCTCCTGCTG ACTCTGGCAA GATGGTAGCA	480
GTTCTCCATA CCCCCTAGAG TCCTTGAGAA GCCTGTCCAA AGCTCTGACT TGAGTGGTAC	540
TCCAGCCACT ATACACACTG CACAATCTCA TTGCTGGAAA ATTGTTGCAG TGATCAACGG	600
TGACTTTGCA GAGCAGTGCC AACCCATATCC CCTAGT	636

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

CTCTAAAACG	AATTCTCTAC	AAGCACCGCA	AGGGCATGGC	TGAACTTCCA	CCATAAGGTG	60
GTTTGTCTCG	AAAGGCTAAT	ACTTCNTTAA	CCTTAGTTTG	TCCTGAAAAT	TGGTACATAT	120
TGAAGAGGGC	CGCCCGTTCT	GCGCAGAGAT	GGAAAACACC	ACAGGTTCCT	TCCATACAGA	180
ATCCTGTAAA	TATTTGTCCA	TCTCCTGCTT	CTACTGCAGC	TACAACATGA	TTGGCATAAA	240
CAAAGTCTGA	TACTTCATGT	GGATTGTATA	GTTTCTGTGC	TTCTTCCTAC	ATCTTTTCCC	300
AGATGTCCAT	TATTGTATCC	TCTATATTTA	GAGATTTCTT	TTAGAATGTT	TTGCATATGC	360
TGAATTGATT	TTTCACGTCC	AAGCAAGAAA	ATTGTATCTG	GTAATTCTGG	CCCATGCATT	420
TCGCCTGAAA	CTGCGATACG	AATAGGCATG	AAAAGATTTT	TCCCTTTAAT	ACCTGTTTCT	480
TTTTGGACTG	CTTTAATTTG	CGGGAAGATA	TTTTCTGTCA	CAAATTCATC	ATCTGTCATC	540
CGCTTCAATT	TTTGCTTTGA	ATGCTTCAAG	AACTGTTGGA	ACTGTTTCAC	CCGTCATGAC	600
TTGCGCTCT	GCTTCTGTCA	ATTCCTGGGA	AATCTGAGAA	GAAAGATCTG	TCCATGGGAT	660
ATCTCATCTA	CTGATTCATT	GTGGTTTATA	GAG			693

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

CTGACAAAGG	AGACGGGTAT	GGAACAAACA	TTCTTTATCA	TCAAACCAGA	TGGTGTA AAA	60
AGAGGGCTAG	TGGGTGAAGT	GTAAAGCGC	ATCGAACAAC	GTGGATTTAC	AATCGAAAAA	120
TTGGAGTTTC	GTTACAGGT	TTTCAGAAGA	GTAGATTGAC	CAGCACTATC	AGGACCTGGT	180
TGGTCAGAGT	TTTTACCCAC	CGATTCTGTA	ATTCATGACT	TCAGGTCCAG	TTCTGTGGG	240
TGTCATTTCT	GGTCCCAAAG	TAATCGAAAC	TTGGCGGACC	ATGATGGGTG	CAACTCGTCC	300
AGAAGAAGCT	TTACCAGGCA	CTATTTCGAGG	TGATTTTGCA	AAAGCTGCTG	GAGAAAATGA	360
GATTATCCAA	AATGTTGTAC	ATGGTTCAGA	TTCCGAGAAG	AATCAGCTAA	GCCGAGAAAT	420
TGCTCCTTTG	GTTTTAAGAG	TGGATTGGCT	CAATCAATTG	GATAAAAGCT	CATTTGAATA	480
GAAAGTATAG	TCAATTAGTT	TAAGAÇATGA	CGCATGATAT	CAAAC TTTT	AGTTTTTGAT	540
ATGGTGC GTT	TTT					553

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

CTAGAGATTT NCGAAGAGTA TTATTGTACT TTAAAGGTCT TGAGATAATT GTCTTTNCCT	60
ACTTGACCTT CGAAGGTTTT ACCATTTTCA AGGTAAGGAA GGTCATCGGA TACTGAAGCC	120
TTGACCTTGT ATATCTTGCC ATCAACTTTA AAGAAGTAGA CAGTGTCTCC CTTGATAACA	180
GCTGATTTGA GGTCTGCTAC TACTCCCTTG ATGCTTTCTG TCGTTGCATT GTCAATTCA	240
AGGTCGTTTT TATTGGCATA CTTGCTGAGC ATCTCTTCCA CTGTAGTAGC AACGATAACA	300
TTTGGTACT CGACTGCGTC TACCAGGGCG TACTCTTTGA CCAAGCCAGC ATTGTCCTTT	360
AAGCCCATGA TGTAAGAGG CTTGTCATTG AGGTTGATAA AGATTGGGGA AAGGTTGCTT	420
TGTAGGATTT CTCCTGAACA GCACCTTCTG CTGATTCACG GGCTGATTCT TCTGTCGCAG	480
AAGCCAAG	488

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

TACAGCTATC GGGTCCGTCT GGTAGTTGGT CCTCAGAACC TTCACTGCCA CTTCTTCCCC	60
ATCTAAGATT AAGTCTTTGG CTAGGTAGAC ATCCGCCATG CCTCCTCGAC CAATCTGTTT	120
GACAATCCGA TAGCGTCCGG CAAAATCTT GCCGATTTGG ATCATTCTTC ATCCTCCTCG	180
TTCATAGAAA CAAGGGCAAC CGTAATGTTG TCTAAACCTC CTGCATTGTT AGCAAAACGA	240
ACAAGTGTCT CCGTTTTATC TGCTAAAGGA ATATCACTGG TTACAATATC ACGAATCTCA	300
CTGCCTGAAA TCATGTTGGT CAAGCCGTCA CTATTGAGCA AGAGATAGTC ACCTGACTCA	360
AGGATAACTG TCCCAAAATC AGGCTGAATT TCATCTTTTT GCCCAATAGA CTGGGTGATA	420
ATATTTTTTT GTGGATGACT TCTGCCTCTT CTGGTGTCAA TTGACCAGCC TTGAGCAATT	480
CATTAACCAA AGAATGATCG CTCGTCAACT GATGGTATCT TCTCCACGAA TCAAGCCGAT	540
ACG	543

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

CTTTAAGGAA AATCAAATCT CTCATGCTGA TACCTCTCCT CATTAAATTA AATAGTAAAA	60
AAGATTCTAT CTCACTCCCT GATTATTACA AAACCATTGA AATATCACAA CTAATAGGCT	120
AGAATGGACA TAGTAAGATN TAGTAGATGA GTCATTCTAC TCAAATCCAC GTTAGAAAGG	180
ACTGCTATGC CAGACAATCT CGCGCTTCGC ATGCGCCCTA AAACCATCGA CCAGGTCATC	240
GGTCAGGAGC NTCTGGTCGG ACCTGGAAAA ATCATCCGCC GCATGGTGGG AGCCAACCGC	300
CTGTCCTCCA TGATTCTATA TGGCCCTCCT GGAATCGGCA AAACCAGTAT TGCCTCTGCC	360
ATCGCTGGAA CGACCAAGTA TGCCTTTCGA ACTTTCAATG CGACAGTTGA TAGTTAAAAA	420
GCGACTGCAA GAAATCTCGG AAGAAGCTAA ATTTNCTGGT GGTCTCGTCC TATTGCTAGA	480
CGANATTCAT CGACTAGATA GACC	504

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CTAATAGAGG CGAAAAAATT TCAGGTCCTC CTTTGCTAGA TGATAATGAG GAAACTAAGA	60
TTTTACCAAC CTCTTCTTCC CGTTTTGGTT ATGCCAATCC TAAGGATCAT GGTTTTAGCC	120
AGGAAACCTT GAAGATTCAG GTCGAACCAT CTATTCATAA AAGCCGTCGT ATTGAAAATA	180
CCAAGAGAAA TGTCTTCAAT TCTAAGTTGA ATAAAACTTT ATTTGCGGTC ATCTTTCTCT	240
TGATTTTGCT TGTTTTAGCA ATGAACTTT TGTAATAGAA AAGGAATTGA AATGAAAATA	300
GGAATTATTG CTGCTATGCC AGAAGAAGT GCTTATCTGG TCCAGCATTT AGATAATGCC	360
CAGGAGCAAG TTGTTTTGGG GAATACCTAT CATAAGGAA ACCATTGCTT CTCATGAAAG	420
TCGTTCTTGT TAAAAAGTGG AATTGGTAAG GTCATGTCTG CTATGAATTG TGTGGCGAAT	480
TTTGGCTGAT CATTTCCAGG TTGGATGCCC TTATTAATAC GGGTTCAG	528

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CTAATAAGAC	TGAAAAGAAG	TCCAGCCAGA	TGTCCCTAAA	AATACAGAAA	AAACATTAAA	60
ACCAAAGGAA	ATCAAATTTA	ATTCTTGGA	AGAATTGTTA	AAATGGGAAC	CAGGTGCTCG	120
TGAAGATGAT	GCTATTAACC	GCGGATCTGT	TGTCCTCGCT	TCACGTCGGA	CGGTCAATTTA	180
GTCAATGAAA	AAGCTAGCAA	GGAAGCAAAA	GTTCAAGCCT	TATCAAACAC	CAATTCTAAA	240
GCAAAAGACC	ATGCTTCTGT	TGGTGGAGAA	GAGTTCAAGG	CCTATGCTTT	TGACTATTGG	300
CAATATCTAG	ATTCAATGGT	CTTCTGGGAA	GGTCTCGTAC	CAACTCCTGA	CGTTATTGAT	360
GCAGGTCACG	TAACGGGGTT	CCTGTATACG	GTACACTCTT	CTTCAACTGG	TCTAATAGTA	420
TTGCAGATCA	AGAAAGATTT	GCTGAAGCTT	TGAAGCAAGA	CGCAGATGGT	AG	472

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

CTTTTAAATA	AGAAGAATCA	CACTCATTGC	TAAATGTGAT	ATAATATTGT	TCTCAGTCTC	60
AGCAGTGCGT	TGTGAAAAAG	CCATACTAAT	CCCTGATTTT	TCCGCATATT	CCATCACCTC	120
AAGTGTTTTA	CTCACTGAGC	CAACTTGATT	AGGCTTTATT	ACAATACCAT	CAGCACAATC	180
TTTAAACTGT	GAAATTCTTT	CTAAGTTTGT	TGCGTAAAAA	TCATCACCAA	AAACTTGTA	240
CTTTAGAGGT	TTTATCAATT	GAAATTTTCT	CCAACTATCC	AAATCTTCAT	CGGAAAATGG	300
ATCTTCAAGA	TAAACCAATG	GATACTTAAC	TCCCCAATCA	CAATAAGTAT	CCATAATTTC	360
TGTGACTGTC	TGTTGCTGAC	TAACACACCA	TGGTACTTTA	TATATGCCAA	GTGAAGAATC	420
GTAACGATCT	GTCATTGCTA	AATCTAAACC	GATATCATAT	CTATTTTGT	ATAATTTTAA	480
TGTCTCTAAT	AACGAATCCA	AAATAATATA	AAAATCATCC	GTGTTAATTA	TTAATGCACC	540
TTGATAGAAA	TAGATGTTGT	AGAAACCTGG	GTTTAACTT	TATCATAACT	CATTTTATG	600
TTAGA						605

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

CTGAAGAAAA TCAGTAAACA AGAGCTGGTT AACACGCGCT TTTCTCGTTT ATTTGCTCAT	60
TTTGGACAGG AAAAAGACGG TAGTTTTCTT GCCCAGCGTT ACCAATTTTA CCTCGCCCAG	120
CAGGGACAAA CACTATCGGG CGCTCATGAT CTCTTGGACA GCCTCATTGA GCGTGATTAT	180
AACTTGATATG CTGCGACAAA TGGCATTACT GCCATTCAGA CAGGACGTTT GGCTCAATCT	240
GGTCTAGCAC CTTATTTCAA TCAAGTCTTT ATCTCAGAAC AGTTGCAAAC TCAAAAGCCG	300
GATGCTCTTT TTTATGAAAA GATTGGCCAG CAAATTGCTG GATTTAGTAA AGAAAAGACC	360
TGATGATTGG AGATTCTCTA ACCGCCGACA TTCAAGGTGG CAATAATGCG GGGATTGACA	420
CTATCTGGTA TAATCCTCAT CACCTCGAAA ATCACACACA AGCCCAGCCG ACTTACGAAG	480
TCTATTCTTA CCAAGACTTG CTGGATTGTT TAGATAAAAA TATTCTTGAA AGATCACGTT	540
TTAAGGAGAT AG	552

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

CTTTGTCTGT ATCTGCCTTT TTATGCTATA CTTAAGGTAT GCATAGAAAA ACAGTGATTG	60
ATTNTAGGAC TTTAGGGGAG AGATATACCT TTACCCANCC TATTAAAGAG TTGAAAACGA	120
GAAATGTAGC AGAAGTGGCA GATTTGCTGG CACNAGTGGA AAGCTACCAA GAGCAAGATT	180
ATTATGTGGT GGGGTATGTC AGCTACGAGG CTGCACCTGC TTTTGAGGAG AAATTAGCAG	240
TTCACAAGGT TCCTCTACTG GGCGAGTACT TGCTTTACTT TACTGTTTCA GATAGGGTGG	300
AGACCTCCCC TATTCCTCTG ACTTATGAGG ATATTGATTT GCCCTCAAAT TGGCAGGGAA	360
NTAACGTCTG CACAGAACTA TGANAAGGCC ATTGCCCAGA TACAC	405

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

CTCAAAAACA	GCTTCTAACA	GCTTGAACAA	GGGGGCTAAA	ATTGATTCCCT	TGATGTAGGG	60
TTTGAAGTAA	GATAATAGGT	GTTTCATAAA	TCCCTTCTAT	TCATATTCTA	GAAATGAAGA	120
AAGTGGGAAG	CCCCACTCTC	TGTTTTATTT	GTTTAAGTAA	GGCAATAGAT	AGCCATATCC	180
TGCTTTTTC	ATCTCATCCT	TGGCCACAAA	GCGTAAAGAA	GCAGAATTGA	TACAGTAACG	240
GAGGCCGCCT	AACTCCCGCG	GTCCATCTGT	GAAAACATGA	CCCAAGTGAG	CACTGCCTGA	300
ACGAGAACGA	ACTTCAATTC	GCTCCATTCC	ATGGCTCAGA	TCCTTGTAAT	AATGAATCAA	360
CTCTTTGGAA	ATCGGACGGC	TTAAAACTTG	GCCAACCCAC	AACCTGAAGC	AAACTTATCC	420
TTGGCAAAAA	AGAGTTGGCT	CACCTGTTCG	TAATATCTAC	ATAAATCCCC	TCCTTCCAAA	480
GGTTTTGGTC	CATAGGCATT	GGTAAATGGA	CCTCCTGTTA	CCAG		524

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

CTTCATCTGG	TGGTTCTCCA	GTTGTAAGTA	ACGTAGTACC	ATTCTCAAAA	CCATACTCAC	60
AAGTTGGTAT	TAAGGGGGAA	CCATATATCT	TTAAAGGAAT	GAAATTGCAA	AAAGATATTG	120
TTACAACAAA	AGAATATAAC	GAGGTTTTAA	AAAATGGCAA	AAAGAAAAAT	TGGAATCCAA	180
TAGCAAATAC	CAAAAAGAAC	TAGAAAAATA	CATTAAATAA	GGAATGGTAT	TGATCTTGAT	240
AAAATTTTTA	AAATACTGTC	ATTTTGAATA	TAAAGGAGTT	TGATATGGAG	TGGATTAGAT	300
TAATAGGAAT	AGCAATCATT	GTTGTGGGTT	TTATTTTAAA	ATTTGATACA	ATTGCAACAG	360
TAGTCTTAGC	TGGTTTGGTT	ACAGCTTTAG	TTTCAGGTGT	TTCTCTCGTT	GAATTTTTGG	420
AGATTTTGGG	AAAAGAATTT	AGCAATCAGC	GAGTGCTCAC	GATTTTTATG	GTTACCTTGC	480
CTCTTGTTGG	GCTGTCAGAA	ACCTTTGGAC	TCAACAACGA	TCAATCGATT	TGATTCGAAA	540
GATTAAAGGT	CTGACAGTTG	GAAACTTCTA	TACAGTTTAT	TCTTTATCGA	GAG	593

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

CCTGCTCCTT	ATCTTTGCAG	TAATTGGCGT	TTTAGTGGCC	TTGATAGCTC	AATTTTACTC	60
AGCAAAGGCA	GCAGTAGGTT	TTGCTAAGGA	ATTGACAAAC	GATCTTTATC	GTCATATTCT	120
TTCTTGCCC	AAGGACAGCA	GAGACCGTCT	GACAACTTCT	AGTTTGGTTA	CTCGCTTGAC	180
TTCCGATACC	TACCAGATTC	AGACTGGTAT	CAATCAATTC	CTGCGTCTCT	TTTTACGAGC	240
GCCCATTATC	GTTTTTGGTG	CCATTTTAT	GGCTTATCGA	ATCTCAGCTG	AGTTGACTTT	300
CTGGTTCTTA	GTCATGGTTG	CCATTTTGAC	CATTGTCAAT	GTTAGGGTTA	TCTCGATTGG	360
TCAATCCTCT	CTACAGTAGT	CTCAGAAAGA	AAACCGAACC	ACTGGGTTC	NGAAACCCCC	420
CNCCATTGCA	AGGATGCCGG	GTTATTCGGT	GCCTTT			456

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 565 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

CTTGACAGT	TGAATCGTTC	AGATATTGAT	TTTGAAAACA	GAGAGTGTGT	TGTCTTTGGT	60
AAAGGAAAGA	AGGAGAGACC	AGTATATTTT	GACGCTCGGA	CGAAAATTCA	TTTAAGAAAT	120
TATCTTAACG	ACAGAAAAAG	ATAGTCACCC	TGCTCTTTTT	GTAACGCTAG	TTGGAAAAGC	180
CCAGAGACTT	GGAATTGCTG	GTGTAGAGAT	TCGCTTAAGA	AAGTTAGGAG	ACAAACTCGG	240
CATACAAAAG	GTTCACCCAC	ATAAGTTCAG	AAGAACTTTA	GCGACTAAGG	CAATTGATAA	300
AGGTATGCCT	ATCGAACAAG	TCCAAAAACT	GCTAGGTCAT	AGCAAGATTG	ACACAACCCT	360
GGCCTATGCC	ATGGTCAATC	AAAATAATGT	CAAGCATTC	CACCAAAAAT	TCTCTCTTA	420
AAAGCAAATC	CCGATATTCC	GAAGAGGTGG	TTGCATGAAG	AAAGTGAAAT	TAGGTGAAGT	480
GGCTACTTTT	ATCAATGGCT	ATGCTTTTAA	ACCTCAAGAT	TGGTCCTCTG	AAGGAAAGAG	540
ATTATCCGAA	TTACCGAATC	TGACT				565

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 538 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

CTTTATACTT	TATCATTCT	AACTTAATTA	TAGTCTTATT	TTTAATAAAG	TTCAATTATT	60
TATATGTAAA	ATTCCTCATC	AGTAAAAAAT	AACCGATCTC	ATTTCTGAGA	ATCGGTTTTTC	120
TAAATAAATC	AAACCGATCA	TTTACATAAC	ATAAATTATG	TAAATGATCA	TACTACAACA	180
ACAAATCTTT	GACTTTTCCA	ATTTCACTTT	TTGGAATAAC	CAGGTGAATC	ATATCACCCA	240
GATACATTCT	GGTTGAGCCG	TTAACTGTTT	GGCTCTTGCC	ATTATGGACT	TGAGTTGTGA	300
TGAGGACGTT	GTGTGGTAAG	TTGAGTTCAT	GAAC TTGTTT	CCCAGCAATT	TTATCAGAAA	360
CTGGTATTTT	GATAAGTGTA	ACTTCTCCTT	CGCTAGATAC	TTCTTCTGGG	AAGCATTTTTT	420
TCCAGCATGG	CTTCATAGAC	TGGCGTTTCT	TTGAGCNAAT	CCCTGATNAT	TTTAGAAAACC	480
AGAGTGACAG	ACCAGTGGCT	TAAGGTGCGA	ATATCTCCTA	CCATCTCAGT	TACGAGAT	538

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

CGTGCTAACC	ATGAGAGCAT	ATATTTCTCT	CAACTATTTT	TATTTCAAAA	AATCCTTACT	60
ATATTGTATC	ACAATCAGAC	ACAAAAAGAA	AAAGCAAATG	ATAAACAAAT	GCTTTTAANG	120
TTTTAAAAAA	AGCTTCGAAA	GGTTCTTCTT	TATTTTTTAA	NGGGAGAGAT	AACGTTGATA	180
TCTAAATCGT	GGTCAAAGCC	GGCAATTTTC	CTTTAGATGT	GTATTGGTGA	ATATCATAAT	240
CTAAATCAGT	TTTAGGACTG	CTCTCCAAAA	ATCCTGAGTC	TGAGCCGTAG	GACGGAATCC	300
AAACAGAGGT	AAACTTGCCT	GTATCAATAC	TGTGTTCTTC	CATGAAGTAG	ACACCAACGT	360
AGATGCCGAT	GTTTTTAGCA	CCTAGTGATG	CTAGTTTTGC	TCGAAAGTTT	TCGACACCTT	420
CGTTCATATA	GACATAGTTT	TGTCTCCACG	TCAGCCCAT	GTAAGTAGGC	TGTTAGGAGA	480
GCACATTGTA	GAAAACTTCG	GCAGCCTTT				509

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

CTGTTCTGTT	TGCGACGCTA	CTTGGTTGTA	GCATGGGGGT	GGTTTTAGAT	GGTCAGTAAG	60
TATCTTTTAT	TAGCAGTTAT	TTTCTCTGGC	TTGGTGACTT	GGATTCTCCG	TATGATTTCC	120
TTCATCTTAG	TCAAGTATAA	GGGCTTGCCT	GCAATCGTTG	AGCGTTTTTT	GAAGTTCTTG	180
CCCGTTTCCA	TTATCTTTGC	CTTGATTCTT	TCAAGCGTAG	TGACAGGTAA	GGTTGGGAGC	240
CTTCCTCAAA	TTAAATGGCT	AGACTTCTTA	GCCGCTTTTC	CAACAGCTTG	GGTAGCCTTT	300
CGCTACCGCA	ATCTACTCGG	AACAGTTCTC	TTTGGAGTGG	TCTTGATTGC	CATCTTGCGT	360
TTGGTCTCTT	AAATTACCCA	CCAAAAAAC	TTATCACAGA	GATAGATATC	ATATAATGGC	420
GTAAATGCTC	CTTTTCTGTT	AAGATTATAA	GGTATTCTAT	TTTGGAGGAA	ATGACATGAA	480
AAAAATCGTT	AAATACTCAT	CTCTTGCTGC	CCTAGGACTT	GTTGCTGCAG	TGTGCTTGCG	540
GCTTGCTCAG	GGGTGCTCAG	AAAGAAGAGA	AC			572

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

CTAGGTTATT	TAGTAAAAGA	CTAGAAGATT	TTCTTTTCCC	AATCGTCTTC	TGTACGGCGA	60
GGATAGAAAA	ACTCTGACTT	GTCGGGAGCT	TCCATCATTT	CCATCAATGG	TAGCATATCA	120
TAGGCCAGAT	TTAAGTTTGG	AATCTGGTCT	TTTTGCACCC	AAGAACTTC	TCCCTCTTCT	180
GAAGATTGAA	GGGTACCAGA	GAACTCAGTC	GCCTTATAAC	AAATGACAAT	ATAGCGCCCA	240
CCTGTATCTA	GTGGCCAATT	TTTAATGCCG	ACAAGTTGAG	GATTTTGGAT	AGTCAACCCT	300
GTTTCTTCGT	AGATTTACAG	AATGACAGAC	TCCGCAAAAG	CCTCATCATT	TTCTACATGA	360
CCTCCAGGAA	AGGCATAACC	AGACCAGCGA	TTGTTTTTCA	GGGCGCGATA	CTGCATCACC	420
ACGCGCTGAG	TTTCGANGTC	TTCCATCAGA	CAGATATTTG	TTTAAATTGT	TTAATTGGGA	480
ACGGGACATA	AATTTAC					497

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

CTGAAATTTT	GGAAGAAGAA	ATCGGTGTAG	ATACAGTCCA	AAAAATAGGA	CGCATCTTGA	60
TTTTGTTTAA	ACAATCTAGC	AAGAAAGAAA	ATCGCAAGAT	TTCTAAGAAA	GTCAAAGAAA	120
TCTAAGATCG	AAACTCCAAA	TAAGTGTTTT	TATAGAGAAA	TAAAGGGGAC	TAGCCTATGA	180
CAATCGAACT	ATTGACTCCC	TTTACCAAGG	TAGAGTTGGA	GCCAGAAATC	AAGGAGAAAA	240
AACGCAAACA	AGTTGGGATT	TTAGGGGGGA	ATTTTAACCC	TGTTTACAAT	GCCCATCTCA	300
TTGTTGCGGA	TCAAGTACGG	CAACAGTTGG	GACTGGATCA	AGTTCTGCTC	ATGCCTGAAT	360
ACCAACCTCC	TCACGTTTGA	TAAAAAGGAA	ACCATCCCTG	AACACCATCG	TCTCAAGATG	420
CTTGA						425

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

CTGCTATCAA	GACAGTATTA	CCGCTGAAAG	AAACAGCTTC	ACTAGAAGGC	GCAATTGAAA	60
AATAAGACGG	GATCACGAAC	TCCCGTTTTT	CTATAAAAGA	AAGGAAATGG	GATGAAAAAA	120
TTAGTCTTTG	TCTGTCTGGG	AAATATTTGC	CGTAGCCCTA	TGGCCGAGTT	TGTTATGAAA	180
TCAATGACAG	ATAACTACGA	AATCCAAAGT	CGAGCAACTT	CCTCTTGCGA	ACATGGCAAT	240
CCGATTCATA	AGGGGACTCA	GCGAATTTTT	CAAGAGTATG	AGATTCCTTA	TGACAAGAAC	300
AAGACATCGC	TTCAGATTAG	TAAGGAAGAT	TTTGAAGCCT	TTGATTATAT	TATCGGAATG	360
GACGCTTCAA	ATGTTCCGAC	TTACGTCAGA	TGTGTCCAGT	AGACTGTCAA	GATAAGAT	418

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

ACTGTTTGAA	AAATATGATT	CGTGGTCGAG	AAATGAATTG	CATTTAAGCA	ATGTAGTTCA	60
GTATATAGAT	TTGGAAATTA	ATGATTTAAC	AAAATAAAGG	AGAAAAACA	TGGTTAAATA	120
CGGTGTTGTT	GGAGCAGGGT	ATTTTGGAGC	TGAATTGGCT	CGCTATATGC	AAAAGAATGA	180
TGGAGCAGAN	ATTACTCTTC	TCTATGATCC	AGATAATGCA	GAGGCGATTG	CAGAAGAATT	240
GGGAGCAAAA	GTTAGCAAGT	TCCTTAGATG	AGTTGGTTTC	TAGCGATGAA	GTTAGATTGT	300
GTTATCGTCG	CAACTCCCAA	ATAATCTTCA	TAAGGAACCG	GTTATTAAGG	CTGCACAGCA	360
TGGTAAAAAT	GTTTTCCTGT	TGAAAAA				387

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

CTTATGAAAT	CAATCATCAA	AATAATATTG	ATCAGGACTA	TTAGGTAAA	TTATCTACAA	60
CGATTAAATT	GGTAGCAGAA	AAGGAAAATG	CCGTTGAGAT	CCTAGAACAC	TTGAATGTTG	120
TCCCTGTGTT	GACAGCCCAT	CCAACACAAG	TGCAACGCAA	AAGTATGTTG	GATTTAACAA	180
ATCATATTCA	TAGTCTTTTG	CGTAAATACC	GTGATGTAA	GTTGGGGTTA	ATCAATAAAG	240
ATAAATGGCA	CAATGATTTG	CGTCGTTACA	TCGAAATTAT	CATGCAGACA	GACATGATTC	300
GTGAGAAAAA	ATTAAAAGTG	ACTAACGAAA	TCACGAATGC	TATGGAAATA	TTACAACAGC	360
TCCTTTTTGA	AAGCTGTCCC	TCATTTGACG	ACGGAGTATA	AGCGCTTAGC	GCAAGCGCAT	420
GGTCTGAATT	TAAAACAGGC	TAAACCAATC	ACCATGGGTA	TGTGGATAGG	TGGTGACCGT	480
GAAGGAAATC	CATTTGTTAC	AGCAAAGAAC	TTGAAGCAGT	CTGCACTCAC	TCAGTGTGAA	540
GTCNTCCTGA	ACTTACTATG	A				561

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

CGACCTAATC	ATATTGATAC	TGCATTTGCA	TCAGCAGATT	TGTTTGAGTA	TAAATTACAA	60
TTAGCAGGAC	AGACTTGGGG	ATATTTAGAA	TTTGAAACAA	ATACAGAAAA	ATATGGGAAA	120
GTATTGTAA	TTATAAGGG	TAAGAAGCGA	CTTACGAACC	AATTTCTTT	GGTACAAAA	180
AATAAGAGTG	GCTACTTATT	TGAATATGCT	CAGATGAATA	CACTTTATCT	TAATCAACAT	240
TCTTCCTACA	AAAATGATGA	AGATAGTCAT	TCCTTTCCAA	TTCAGATGGA	GTTAGTTTCT	300
GATGAAATGA	TTCCAAGAAA	TTGAACAAGC	TACTAAAAAT	TCCGAATATC	CGAAAAATTT	360
ATGATTTTAA	CTTATGANGC	GGACTCCCGA	AAAACAATAT	TATATCTGTT	AGATGTTTGT	420
TATGCCCTGA	TGCCCCGAAC	GGTCCAGTTA	CACTTGATTC	CAGATTGTCC	TGAGTATATC	480
CATCCAGTTC	CGTACC					496

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

CCACCCTCTA	GCAAGTGGTG	CTAATTCCTA	TAGCCTAGAA	GAAAACGAAA	TCATCTACCA	60
AAAGTTAAAA	AACTTGCTTA	AAAAGTATA	AAATACTTGC	CAAACCTTTC	AGAATCTGAT	120
AGACTAGTAT	GGTAACAATC	TATGGCTCGC	AAAGAGACCA	TGGCAGAAAG	GAAATATTGC	180
AAAATGAAAA	AAGATATCCA	TCCAGAATAT	CGCCAGTTG	TCTTCATGGA	CACAACTACT	240
GGTTACCAAT	TCCTTAGCGG	TTCAACAAAA	CGCTCTAACG	AAACAGTTGA	GTTCTGAAGGC	300
GAAACTTACC	CATTGATCCG	TGTGGAAATT	TCATCAGACT	CACACCCATT	CTACACTGGA	360
CGTCAAAAGT	TCACTCAAGC	AGATGGACGC	GTGGATCGTT	TCAACAAAAA	ATACGGTCTC	420
AAATAATGAT	AAGAGAACAG	TTTCGGCTGT	TCTTTTTTGT	TTCTTGAAAT	CAACTGCTGT	480
TTTCATGTTT	CAGACTCATC	TGTA				504

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

CTCAGGCGAT TACTAATTAC ATGACTTCTG CCTCAAACCTT TAATGTCGAT GAGGCTAGCC	60
AATTCATTCA ACAATTTACA ATTACAAAAC AAATCGAACA AGTAGAAAAA CTATTAGAGG	120
AGTAGCATGG AAAGTGCATT AATTAGTGTG ATTGTGCCAG TCTATAATGT GGCGCAGTAC	180
CTAGAAAAAT CGATAGCTTC CATTGAGAAG CAGACCTATC AAAATCTGGA AATTATTCTT	240
GTTGATGATG GTGCAACAGA TGAAAGTGGT CGCTTGTGTG ATTCAATCGC TGAACAAGAT	300
GACAGGGTGT CAGTGCTTCA TAAAAAGAAC GAAGGATTGT CGCAAGCACG AAATGATGGG	360
ATGAAGCCAG GCTCACGGGG ATTATCTGAT TTTTATTGAC TCAGATGATT ATATCCATCC	420
AGAAATGATT CAGAGCTTAT ATGAGCAATT AGTTCAAGAA GATGCCGATG	470

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

CTTATACTTG CTTTTTTCCT TTTGAAAAAT GTTAATAAAT CGTTGGTAGT CTTCTCTAGG	60
CATGGACAGA TCAATATCGT CGTCCCAAGG GATAAAGCCC TCATGTCGAA CCGCCCCAAT	120
CAGAGTACCG TAGTTAATAA TATAGTTGAT ATTGTGCTTT TTACAGAGAG TATCAATATA	180
ATCCAAAATT TCTAATTCAA TTTGTTTGGC ATCTTCAATG GTTAGTTGTT TCATTTTAAA	240
CTCCTATGAT TTTTTGAATT TATTTTTTAA GGCTAGGACA TGGTTTAAAA ATTCATAGAA	300
AATGCTATCT TTTGTGAAGA CAAGTAGACT AATATAAGAG ATAGCTGATA ACAAGACAAT	360
CAAACCAGTA TTAATCAAAA ATGGCAAATT AATGACCATA TCCACAGGAT ACACGAAATT	420
AATCAGGAAA TACATTGCTA CAAAGGAAAG TGAAAAGAGA GAGTATCGAA CAGTATAGCT	480
AAAGATATGT CCAAGTGGA TGAGTTGTTT CTATGGATGA AATGAT	526

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

ACCATATCAA	TACTATCGAA	AAGTACAAGG	GATNCAGTCT	CAAGGTCGCT	GAGGAAGATT	60
TGAATGACCT	AGACGATGGT	GAATTTTACT	ATCACGAGAT	TATCGGTTTG	GAAGTCTATG	120
AGGGTGATAG	CTTGTTTGA	ACCATCAAGG	AAAATCCTGC	AACCAGGTGC	TAATGATGTC	180
TGGGTGGTCA	AACGAAAAGG	CAAACGTGAT	TTGCTTTTAC	CTTATATCCC	ACCAGTGGTT	240
CTCAATGTTG	ATATTCCAAA	TAAACGGGTC	GATGTGGAAA	TCTTAGAAGG	GTTAGACGAT	300
GAAGATTGAT	ATTTTAACCC	TCTTTCCAGA	GATGTTTTCT	CCACTGGAGC	ACTCAATCGT	360
TGGAAAGGCT	CGAGAAAAG	GGCTCTTTGG	ATATCCCAGT	TNTCATAATT	TTTCGAANAA	420
AATGCTGAAA	AGG					433

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

CTGCAACTTG	AATTTCTCCT	TCTTGTTTCA	AAGCAAGATA	AACAATTCTGA	GCCCCCTCTTT	60
TTTCTAGCAA	ATCCCCCATC	TGGACAGATT	GCATAAAGGA	ACGAGAAGAA	ACCTGATCAG	120
AATAAGTCTG	AAACTCTTCT	TCGTGAGTG	TTGTTAGTGC	CATATACTTA	CTTTCTATGT	180
TTTTTTCTTA	ATGTTTTTACG	GAAATCAAGA	GCAAGTCTTA	ACAGAGGATA	GAGAGGATGA	240
GTGGGCATTG	TAAATTCACC	CAAGTATTCT	TCAATCGTTG	GATTAAATTT	TTCCTTAAAA	300
TGATAAAGTC	CACCATTGAG	AGAGTTTTCA	ACACCACCTA	AATTTTGCCA	GACCATACCT	360
CGTCAAAGG	CATAGCGAGC	CGTTTCATAC	CATGTTAAAA	TTGGTGCATT	GTAACGTTTA	420
AAATCATCAT	CCATACCAGC	ATATATATTG	ACAGAGGTAG	TACCAAATTC	CAAAC TCAAA	480
GTACCGCTAA	AGGAATCTCG	CTTGACCTAC	ATCTATATAT	TCCTGCAAGA	AGGTCAATTC	540

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

CTCAGGCTAA AAGAGTCCAC TGGACTCTTT TACTCCGTCC CATAACCAAT GACTTAATGG	60
CGCGTTCAGC TAGATTATTG GAAAGGACCA GATGTCCGTC TTTCAAAATA GTCTTAAAGG	120
TTTCTTCATA CTTGAGGCTG TATTCAATTG CCCTTCCTAG TTTTGAACCC GATAAAACTG	180
ACTGACGCCG GCACCAAGCA AAGAAATCTT CCATTAGGGG TTGGAGCTCT TCTTGACGTT	240
TCTGTAGTCG TTCATCAGCT GACAATGTCT CCCAGTCTCT TTCCAAGGCA AATAACTGAT	300
CACAATAGGC TAATCCTTTA G	321

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

CTTGACCAAA CAAGGCAGTT GGAAATTGAT TTTGGAGGAT GAGAGCGCTG GAAGGGAAC	60
CTTCCCAATC TTGACTCAAG GTCNATATAT CGCAACATTT GACCAACAAG CGCCANCTAT	120
CGATGAAATC TTAAACTAT AATCAGGAGT GGAAGTATGA GAAATATGTG GGTGTGAATC	180
AAGGAAACCT ATCTTCNACA TGTGAGTCA TGGAGTTTCT TCTTTATGGT GATTTGCGCCG	240
TTCTCTTTT TAGGAATCTC TGTAGGAATT GGGCATCTCC AAGGTTCTTC TATGACTAAA	300
AATAATAAAG TGGCANTACT GACAACAGTG CCATCTGTAN CATAAGGACT GAAGAATGTA	360
AATGGTGTTA ACTTCGACTA TAAAGATGAA GCAAGTGCCA CCAGAAGCAA TTAAA	415

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

CTATNAAATA GAGTGGTTCT CTATCTGCCA TGACCACAAA TNAGGACAAT GATACTTCTG	60
AACGTTTCTG CTGCTATCGT AAAAGGACAG CGGGTGAGAC GCCCATGAAT GATCTAACCA	120
GTCATACCCA CGGAGGAAAT TATACATAG CACGTTATCA GGAGGAAAAA TTTTGAACA	180
AACAGTTGTA AAATATAGTC TGCAGTTATC AATGCTTAAT TTTTACAGG CGAAGATAAT	240

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

CTTGTCATCC TCACGAAAAT TCGGATTGTA AAGCACCAAG CCTTGACTCG TGATAGACTG	60
AATCATGCTT CTCTCATGTA CTCCTCAAGT CGTTTCATGG CTTCTTTGAT AGTCTCCATG	120
CTGGCTGCAT AAGATAGGCG GACGTAGCCT TCCCCGTAAC GTCCAAAGGC TGCACCAGGG	180
ATAAAGGCAA CGGCCTTCTT CTGAGCAAAA TCCTTCAGAA AAGCAAAGGA GTCTTGATTG	240
TAGCCCGCTG GAATTTTAGC AAAAATATAG AAGGCACCGT CTGGTTTGAT AATCTCAAAA	300
CCAAGAGCAG TCATTTTTTC GATGATATAG TCCCGACGTT GGATATATTC CTTCTTCATG	360
GGCTCCGCAT CGTTTTTACC AGCCGTCAAG GCTTCTACCG CAGCATGTTG CGCCATGGTA	420
TTTGCGGCAG TGACCAAGTT ACTGGTGACT CTTGATTAAAC TGGGCTGTGA AGGTCNCANG	480
AGCAAAAATC AGCCCCAAAC GCCAACCTGT CATGGCATG	519

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

CTTCAGCTAT TCGTGGGATA TTAGATGTAC TTATTTAGGG GTTGAAATCA TATGAATATT	60
ACCAATTTGT TTTCTATCAA GACAGGATGT GATGAACTG ATAGGCAACT GCAAAAATA	120
TTTTTTTCAGT TGGATTTACA ATTGGGAGAA TTGACAGATC AACTAAGAAA ATTAGATTCT	180
AATTTTGTTT CTCGTAGTCA ATTTGTAGAC ACGTTGGATT TGAATGATGT AGAATATAAA	240
GAAATTTTAA ACTATTTTAT CTTCCATCGT AATGATAGTG AAGAAAGTTT GGTAGAATGG	300
TTATATGATT GGATTTCCAC AAATCGTTAT GAACTTCCCT AAAGAGTTTT CCGATTCCGT	360
ATGGCTCCAT AAATACCCAT GAAAGTGTTA CTGAAGTTTT CCGGAGAATG AATAACTAAA	420
AAACAGTCAT TAGTGACTGT TTTTATAGA AAAGAGTTTT TATATGTT	468

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

CTTGAATAGT CTCATCACGA AAATTGCCAT AACTGATAAA ACCAACCACC TTCACGCCAT	60
CCATCGCAAT CAATGTATTT TCTGGATACT TTTGACTAAA GAATCGACAT CTTTCTAATG	120
TCATTGTATC CTGAAATTCC GCAGGCAAAA GGTCATCATA AGACTCTCTC CACGTTTGCC	180
AGTGAACGAG GGATTTGCCT TCTATCTCTT CAGGAGTTNC CATAGATTTG ATAATAACCG	240
TCATTTATTT TCTCCAGTC TNCTCTCAAA ATACCATATT TAATACTATC AAAATATTTA	300
CCTTGATAAT AACGAACTTT NGGAATATGA GCTNCTTTTT TCATNCTTAA TTTTTCAGCA	360
AGTTTCATCA TACCAAGATT TCCTGACCAA GTTGTCAAAA CCAGATGCTC CAACTCCAAG	420
TAATCCTGAA ACGTCCTATC TATCCACTGC AACATAGCAA CTTTCCCAAT ACCAGTGTTT	480
CAGAATTTTT TATCATAAAT ACCAATTCCC AATCCATCCA TCTTGTTTCC TTTACATACC	540
CAATA	545

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

CTTGATTGTG GAAGAAGTCC GTGATCGCTA TGTGGGCAAA GTCGATGCCG TTTTTCATAA	60
CGGCGATTCT GAACTACGTC CGGATTCTCC ACTTTGGGAG GGCATCCGCG TTGTTAAAGG	120
GAACATGGAC TTCTACGCCG GCTACCCAGA ACGTCTGGTG ACTGAGCTTG GTTCGACCAA	180
GATTATCCAA ACTCATGGTC ACTTGTTTGA CATCAATTTT AACTTTCAAA AGTTGGACTA	240
CTGGGCTCAG GAGGAAGAGG CCGCTATCTG CCTCTATGGT CACTTGCAATG TGCCAAGTGC	300
TTGGTTGGAA GGCAAGATCC TCTTTCTAAA TCCAGGCTCT ATCAGTCAAC CACGAGGTAC	360
CATCAGAGAA TGTCTCTATG CTCGTGTGGA GATTGATGAT AGTTACTTCA AAGTGGAATT	420
TTTGACACGA GATCACGAAG TGTATCCAGG TTGTCCAAGG AGTTTAGCCG ATGATGCCAA	480

GGAGTTGAGA CTTTCTGTTG GGGCAGAGAA CTTTTGA

517

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

CGTAACCATT AACTATGAGG TGGTTTGCCT CCTCAGCGAC CGTATTCCGA GAGAATATTA	60
TTAGAAAAGA AAGGAGTGGA GCATGAATCT ACATCAACCC TTGCATGTCT TGCCTGGTGT	120
GGGACCAAAG TCAGCAGAAA AATACGCCAA ACTAGGAATT GAAAACCTGC AAGATCTCTT	180
GCTCTACTTT CCTTTCCGTT ATGAAGACTT CAAAACCAAG CAGGTGCTGG AACTAGAAGA	240
CGGTGAGAAG GCAGTTCTTT CTGGTCAGGT AGTGA CTCT GCTAGTGTCC AGTATTATGG	300
TTTCCAAGCC GCCAATCCGC CTGCGTTTTT AGTCCTCCAA GCCAGGGAAG AAGGTTCTGT	360
TTTTTTTGGC GGGTGAAATT TCCTTTTTTA CCCAGCCCCC TATCCTTGGG CTTGAATAAA	420
AAATTAGAAA TTTTGGGGAA CCAACCCCTT TGGCTTGT	458

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

CCTTACTAGT TTA CTCAATC TTTACATCGT TCTTTCGGCA GTTCAA ACTC AGAATCCACA	60
GCACAGGTTA TGCAATTACT GTCTGAAAAT ATGTTAAAAA CCATTCAGTC ACTTTCGGTC	120
TGGCAGATTT ATTTGCTTGG TTTTGAGCGA ATCTTGGCGC TTGGTTTCCA ATTACTTTTG	180
ACAGTTTGGG TTTACCAAGC TGTTCCGCCAG AAGAAATGGA TTTATCTCCT AGCAGCCTAT	240
GGCTTGCATG CCTTCTTTGA TCTGGCACCA TCTCTTTTCC AAGTAGGCTG GTTGACAAAT	300
CCAGTCTTGG TTGAAGTGAT TCTAGCACTG GAGCTCGTTC TGGTCGCCTA TGGAACCAAG	360
GAAATCTTTT GTAAAAAATC ATAAAAAGGG GGGAACCTCT TTTTCTTATG CAAAATCCAA	420
ACAAGGTATT TTTATGGTCG TCAAATGTCT CTAAAAATGG TATAATGGAA TGAATTTTGT	480
AAAAGGAAGA ATGACATGTC TGTAAGAGAA AAAATGCTTG AAATCTTAGA AGGAATTGAT	540

ATCCGTTTTA AGGAACCCTT GCATAG

566

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

CTTTGACAAA GAGTATGACA CCTGACCGTG AAGTCATTAC CTTTATTCCT GAAAAATTTA	60
TTGTGGATGG TTTCCAAGGG ATTCGTGACC CACGTGGCAT GATGGGGGTT CGCCTTGAAA	120
TGCGTGTTTT GCTTTATACA GGACCTCGTA CTATCTTGCA CAATTTGCGT AAGACGGTTG	180
AGCGTGCAAG TGTTCAGGTT GAAAATGTTA TCATTTTCACC ACTAGCAATG GTTCAGTCTG	240
TTTTGAACGA AGGGGAACGT GAATTTGGTG CTACAGTGAT TGATATGGGG GCAGGTCAAA	300
CGACTGTCGC TACAATCCGT AATCAAGAAC TCCAGTTCAC ACATATTCTC CAAGAAGTGG	360
AGATTATGTA ACTAAAGATA TCTCCAAGGT TTTGAAAACC TCTCGCAAAT TAGCGGAAGG	420
CTTGAACTG AATTACGGGG AACCTATCCG CCTCTTGCAA GCAAAAAACT CCATTAAAGT	480
TATTGGAGAA TTAACCAGT CAAAGTGACG GAACCTACTT GTC	523

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

CTGTGATTTC AGAGAAGAAA TCAAGTGCTG TAACAGAAGT AAGATGTAAT TGTATGTAAA	60
GGAGACGTCA TGTTAAATAG TATTGTAACC ATTATTTGTA TTGCCCTTAT CGCGTTTATC	120
TTGTTTTGGT TTTTCAAAAA GCCTGAAAAA TCTGGACAAA AAGCCAGCA AAAAAACGGA	180
TACCAAGAGA TTCGAGTGGA AGTCATGGGA GGCTATACTC CTGAGTTGAT TGTCCTCAAG	240
AAATCAGTGC CAGCCCGCAT TGTCTTTGAC CGCAAGGATC CTTCAACATG TCTGGATCAA	300
ATTGTTTTTC CAGATTTTGG TGTACATGCG AACCTGCCAA TGGGGGAAGA GTATGTAGTG	360
GAAATCACGC CTGAACAGGC TGGAGAGTTT GGCTTTGCTT GTGGTATGAA CATGATGCAC	420
GGCAAGATGA TTGTAGAGTA GGTGGAGACT ATGACAGAAA TTGTGAAAGC AAGCTTAGAA	480

AATGGCATTTC AAAAAATCCG TATCCGAGCT GAAAAAGGCT ATCATCCACC CATATCCA

538

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

CCTCAAGAAG TCCGCGATAC TTACGAAAAT ATTTTGTAGA GAATCGAACC GCAAGGTTTCG	60
GTTTTCTTTC TCTTTTGTGC TATAATTTGG TATAATAAAC AGTATGAAAA TCGTATCAGG	120
AATCTATGGG GGACGTCCCC TCAAGACACT AGAAGGCAAG ACAACAAGAC CTACTTCGGA	180
TAAGGTTAGG GGAGCCATTT TTAACATGAT TGGTCCCTAC TTTGAAGTGG GACNAGTCTT	240
GGACCTTTAT GCAGGTAGTG GTGGTTTATC TATCGAAGCA GTATCGCGTG GCATGTCCAG	300
TGCTGTTTTG GTGGAGCGAG ACCGTAAGGC TCAGACCATC GTGGCTGAAA ATATCCAGAT	360
GACCAAGGAA GTTGAAAAAT TTCAACTCCT CCAAAATGGA TGCAGAAAGG GCATTGGAAC	420
AGGTTNTCTG GGGAATTTGA CCTCGTTTTT TTAGACCCTC CCTATGCCAA GGAACAAATC	480
GTAGCAGATA TTGAAAAAAT GGCTGAGAGA GAGCT	515

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

CTGGANACAA ACTTTACAGA TCAAGTCGAT ACGATGATTT ATGTTGATAA AGAAGAAAAA	60
GAAACTATTA AAGCTGCACT TGTGGAGTTT TTTAATGGAA AAGTCACTTT AACTGACCAA	120
GGTTTACGAG AGGTTGAAGT TCCTGTAAAC TTAGTGTAAC CAATGAATAA TACAGCGTTT	180
CGTTGACATT CTCACAACTA CTTTAGCGAG CAAAATAAAA AGATGCGTAC CAAAATATAC	240
TAGAAAATGA AGCAATTCAA ACGAAACCTG ATATCGTTTT CCTTCACACC TATTTACTAG	300
AATTAAGTGA ACGCAATCAC TTGAAATTA ATGACTTTGG AT	342

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

CTATTAGCGA CTTTCTCTGA AATATGGTAT GATAAAGGAT ATACAAGGAG ATAAAAATGAA	60
TAATAATTTA CTGGTATTAC AATCCAGACT TTGGTCTGGT TGATGGTGCG GTATCGGCTA	120
TGATTGGAGT GGCTTTAGAA GAGTCTCCAA CCTTAAAAAT CCATCACTTG ACGCACGATA	180
TCACGCCTTA TAATATTTT GAGGGGAGCT ATCGTCTCTT TCAGACGGTG GATTACTGGC	240
CTGAGGGAAC GACGTTTGTA TCGGTTGTCG ATCCAGGTGT CGGTTGAAA CGTAAGAGTG	300
TAGTTGCCAA GACTGCTCAA AAATCAATAC ATTGTACGCG CAGATAATGG GACGCTTTCC	360
TTTATCAAGA AACACGTTGG CNTTGTANCC ATTCGTGAGA TTTCTGAGGT GGCCAACT	418

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

CTCTCGCTTT TCTCATAGTG GGAGGTAAGG ATGGAATTAC GCAGACCAAG ATTAGCGGAT	60
AAGAAAGCTG TTTTAGATAT GATGACAGAG TTTGAAAAGA GCCAATCAGC CCATGATGGA	120
GGATTTTGGG ATACAGAGAA TTTTGTGTAT GAAGAGTGGT TGGAAAGCAA TCAGGAACAG	180
GAAATGGGGA TTAATCTGCC TGAAGGATGG GTTCCTGCAA TTCAGTTAGT GGCTTTTCT	240
GAGAAAGGTC AAGCAGTTGG ATTTCTTAAT CTCCGGTTGC GCCTCAGTAA CTTTCTACTA	300
GAAGAAGGTG GGCACATTGG CTACTCCATC CGTCCATCTG AAAGAGGCAA GGGTTATGCA	360
AAAGAACTCT CCGTCAGGGC TTGCAAGTTG CTAAGGAAAA GAACATCAAG AAAGCTCTGG	420
TGACCTGTAG CGTGAATAAT CCTGCTAGCA GAGCATCATT CTA	463

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

CTCTTACGTG	ACCAGAACAT	GCTACTTCCC	ATCCGAGAAG	CCATTCTATC	TGGCTTACCA	60
GTGTTTGGA	CCTGTGCGG	CTTAATTTTG	CTGGCTAAGG	AAATCACTTC	TCACAAAGAG	120
AGTTATCTAG	GAACATGGA	TATGGTGGTC	GAGCGTAATG	CTTATGGGCG	CCAATTANGA	180
AGTTCTNCAC	GGAAGCNA	TGTAAGGGAG	TTGGCNAGAT	TCCNATGACC	TTTATCCGTG	240
GTCCGATTAT	CAGTACTGTT	GGTGAGGGTG	TANAAATTCT	AGCAACAGTG	AACNATCAAT	300
TTGTTGCNNC	CCAAGANNA	AATATGTTGG	TAAGTCCTTT	TCATCCAGAA	TTGACTGATN	360
ATNTGCGCTT	GCNCCAGTAC	TTTATCAGTA	TGTGTAAAGA	AAAAAGTNGA	GATTGAATTT	420
CTCCAACCTT	NCCACNTGTA	ATNNNCAATN	NCNATGTATT	GGAGTACGGA	CGCAG	475

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

CCTTCAAAAA	TTATTTGATG	CAACCTTAGA	CAATCCAGAA	CTCACCGCAA	CATTAGTGCC	60
TTTAGGAGAT	GGTATTCTCA	TGCTTCGTAA	AAATGTAGCA	GATGTTCAAC	TGTCTGAAAG	120
CGAATGATTT	TCAGAAAAAT	TTAAGAAAAA	ATAGTAAAT	AGATAGAGTA	ACACTTATCT	180
CAAAGGAGTA	GACATGAAGA	AAAAATTATT	GGCAGGTGCC	ATCACACTAT	TATCAGTAGC	240
AACTTTAGCA	GCTTGTTTCA	AAGGGTCAGA	AGGAGCAGAC	CTTATCAGCA	TGAAAGGGGA	300
TGTCATCACA	GAACATCAAT	TTTATGAGCA	AGTGAAAAAC	AACCCTTCAG	CCCAGCNAGT	360
CTTGTTAAAT	ATGACCATCC	AAAAAGTTTT	TGAAAAAACA	ATATGGCTCA	GAGCTTGATG	420
ATAAAGAGGT	TGATGATACT	ATTGCCGAAG	A			451

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

CTATGGATAA	GGCACTTGCT	GACCTCAAAA	CATCAGGGCA	CTTGCCTATT	CCGCGACACC	60
TACGTGATGG	GCACTACANT	GGAAGCAAGG	AACTGGGGAA	TGCCCAAGAC	TATCTCTATC	120
CACACAACTA	TCCTGNAAAT	TGGGTCAAGC	AAGACTATCT	GCCACAAAAA	ATTCGTAATC	180
ATCACTATTT	CCAAGCAGAA	TATACTGGTA	AATATGAACG	GGCTTTGGCT	CAAAGAAAGG	240
AAGCTATCGA	CCATTTGCGA	AAAATCTGAA	ATCCTTTTCA	AAAAATTGCA	CTTTCCTCTT	300
GATTTTTTTT	GAAAAAGTGG	TATCATATAA	ATATAGAAAC	GCTGTGGTGT	ACGACTTCAC	360
ACTTAAGTGT	TGACCGACTA	TTTTTTGTAT	TATTANGGAA	ACAAAAGTCT	TCTGTCAGCA	420
TGTAGGCCGT	CTCACACGGA	AACAGCTTCA	GTT			453

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

CCGTAGTACA	GGCACAAAAA	GATTTGGAAA	ATAGAAAAAG	AAAAGCCAAG	AAAAAGGCTC	60
AGAAAACGAA	ATAAATAAGG	AGGAATCTGG	TAATGGTAGT	ATTTACAGGT	TCAACTGTTG	120
AAGAAGCAAT	CCAGAAAGGA	TTGAAAGAAT	TAGATATTCC	AAGAATGAAG	GCTCATATCA	180
AAGTCATTTT	TAGGGAGAAA	AAAGGCTTTC	TTGGTCTATT	TGGTAAAAAA	CCAGCCCCAAG	240
TGGATATTGA	AGCGATTAGT	GAAACGACTG	TTGTCAAAGC	AAATCAACAG	GTAGTAAAAG	300
GCGTTCCGAA	AAAAATCAAT	GATTTGAACG	AGCCTGTGAA	GACGGTTAGT	GTAAGAAACC	360
GTTGACCTTG	GTCATGTGGT	TGATGCTATT	AAAAAATAG	AGGAAGAAGG	TCAAGGTATT	420
TCTGATGAAG	TC					432

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

AAAATCAAGA	AATTCTTTGA	AGGAACGACA	GATACAGCTG	AGAACTATAT	CAAGTCGGCC	60
CTTAAAATGT	TGGTCAAATA	GGAGCAGAGA	ATGACAAAAC	GTTGTTCGTG	GGTCAAGATG	120
ACCAACCCGC	TCTACATCGC	CTATCATGAT	GAGGAGTGGG	GTCAGCCCCCT	CCATGATGAC	180
CAAGCATTTGT	TTGAGTTGTT	GTGTATGGAA	ACCTATCAGG	CAGGCCTGTC	TTGGGAAACG	240
GTA CTCAACA	AACGCCAAGC	TTTCCGAGAA	GCCTTTCCAT	AGCTATCAAA	TTCACTCCAG	300
TCGCAGAGAT	GACTGACACT	GAATTGGAAG	CCATGCCTGG	AGAATCCCAG	CTATCATTCC	360
GAAATAGAGC	CCAAGATTTT	TGCTACACGC	CGCCTAACGC	CCCAACCCTT	TCCTACAGTT	420
ACAGGCAG						428

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

CTATTAGATG	GTATTGACTG	CCCAGACACT	TACGGATCTA	GCTGAGACAG	GGAATTGTCC	60
ATAACCTTCC	TCATCAATTG	TAAC TTGACC	TTGGTGGTTA	CCAAGTAAAT	CTACAAAGGT	120
TTGATTAGTC	CATTCTTGAC	CGACAAACAT	TGACTTGCTG	TTTTCTTGGT	CATTTGAAAT	180
CAAGACTGCG	ATTGGGGATT	GATTTTCAGC	ACCTGAACGT	ACCCAACCGA	TACAGTTAGC	240
ATGGTCAAAG	TAGTCATTTT	GTTCTCCATA	GGCCAAATCT	TTTCGGATGG	CTAGGAGGCG	300
GTCAAGGATT	TCTTTGAAAT	CTTGTTGAGC	ATACTGGCCT	GAAATCCCAT	AGTAGTCTCC	360
GTAAAAGACA	CATGGAAGGC	CGTCTTGGCG	TAACAAAATG	AGGGCATAGG	CTGCTGGCTT	420
GAACCATTCT	TCAACGGTAG	ACTCAAGGGC	TTGTCCTCGT	TGGGTATCGT	GGTTGTCGAC	480
AAAATCACAG	ACTTGT CAGG	CTTGAGTTCA	ACCAGGCT			518

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

CTCTGTCTT	TTACCTGAGA	GTTTGAGCAG	TTGCCTGCCT	TGCCCCCTTCG	GTGCCTTTAC	60
GGTCTCTCCA	GAGTTCCGTC	CATTTACAGT	CATGGAAAAT	CAAACGATTC	CCCACCTTCTA	120
TTAAACTTCA	TTCGGTGTTG	GTATTTAATT	GATTCTAATT	TTACAAAAAA	TGTTGGCTTT	180
TGTCAATGTG	TTTATTAGTA	AAAATTAGTT	CAACAGTTTT	TACTTTATAA	AGTCCAGAAT	240
ACTGCTATCC	TTTAAAAGTG	ACAATAGTCG	CACCACTGCC	TCCAGCATTT	TGTGGGGCAT	300
AGCCGAAACT	CTTGACATGT	TTGTTTCTTT	GCAAGTATTT	GGTAACTCCT	TCACGGATGA	360
CTCCTGTTCC	GATACCATGG	ATGATATCAA	CTTGAGCCAT	ATTGTTAAGC	AAGGCTTGGT	420
CGAATGAAGG	TATCTAGCTC	ATTCATGGCT	TCTTCATAGC	GCTTGCCTCG	AAGATTCAGT	480
CTAGCTTGAG	TCCTCGCCCA	GAAGTTTCG				508

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

CTCTTGGGCT	CTCTTCTCAG	CAACTTCCCT	GCTTTCACCT	TTGGTCTTGA	TAGGTGANAA	60
CGTAATATNT	CCAATCANNNG	TCATATTAGG	AAANAGTTAA	ATTGTTGGAA	AACCATGCCC	120
ATCTTCTCAC	GCGTGGGAAA	CAGGTCATTC	TTCTTGTCG	TAATATCGAC	TCCCTCAAAG	180
ATAACCTTCC	CCTTGGTTCG	TTCCTCCAAC	AAATTCATAT	AGCGAAGCAA	GGTAGATTTT	240
CCACTCCCTG	AAGGACCGAT	GATAACGACA	ACTTCTCCTC	TTTAAATCTC	GAGGTTGATG	300
CCCTTCAATA	CTTCATTCTT	TCCAAAAGAT	TTATGTAATT	TTCAATTTTT	ATCAAGGTTT	360
CTGTCATTAT	TTCTTATC					378

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 741 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

CTGGCCAGCC	AGATAAACCT	CGATACGGCT	TTCTGCTCGT	TTGATGCGTT	GCAAGAGTCC	60
GCCCATACGG	ACGTCAACTG	TATCCAAACC	AAAGACCTTG	TTTTATTTCA	GCCAGTGGTG	120
ACTAAAGAGG	GCATGGAAGT	CTTCAATTTG	GCTTCTAAGT	TCTGGTAATT	CTTGTCTGGC	180
GATTTGTTGT	AAACTTTCTT	TATCATCCGC	TTGGTAGGCA	TGACGAATGC	GTCGTCCCAC	240
ATCTACTTTG	CTACTTAAAA	TAGCATTCAA	CTGGGCCTGA	GTTTCAAAGA	GATAAGCATA	300
GTTTCCAGCT	TTTTCTTTAA	TGTCAGCAAT	AGTTCCCGCC	GCCTGAGCGA	AGTGTGGCTT	360
GTCTGTTC	GGTGTCTATG	GTCGGTCAAG	TATCGGACAG	AGAACATCCT	GATAAAAGAC	420
ATAGCGGTTG	GGATTGATGC	CACTGAGATT	ACCTGGTAGG	TCTGGTAAGA	GGTTGGCAAG	480
ATCAATCTGC	ATAAAATCCT	CAACCGTTAG	ACCAGTATTG	GTCTTGAAAT	GCGCAGACAA	540
ACTATCTAGG	TCATTGCGAT	AGATCAAGTT	ATCGATACCG	TCGACCTCGA	GGGGGGCCGT	600
ACCCAGATTT	GCAAGCTTGG	TAGGATAAAG	AACTGGGCAG	TTTCACCACC	ATTGTCTCCC	660
CAACCCGTTA	CGATGACTTC	TTTAATCTGA	TTGGCACGGC	AGGCTTTATT	AGCCTCGATA	720
GCCACTAGAC	GGCTAAAATG	G				741

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

AAACTCGATT	TGAGAGAAAG	TCCAATAAGT	CTTTCATATA	TAAAACGCAT	AGTAGCAAGA	60
GTTTCTACAC	CCACTATTAT	GCGTTTTTAT	CATTTTGAAA	TCTACTGCTA	ATCAATGAAG	120
AAGCAAAGAT	CAAACTAGGC	AGCTAGTTAC	AAGTTACGTA	AGCGCGTCAT	AACAAGGTAT	180
CTATCCTAAT	TCCCCAACTT	CCAGTATACT	AGATAAAAAA	TAATTATCGG	AGGAAAGGTA	240
TTGTACTATG	ATAATTCAAC	TAAGTGATTT	AGGTCAAGTT	CACCTTGTTT	GTGGCAAGAC	300
AGATATGAGG	CAGGGAATAG	ACTCATTAGC	CTATGTAGTT	AAAACCCACT	TTGAATTGGA	360
TCCTTTCTCC	GGTCAAGCCT	TTCTCTTTTG	TGGTGGACGT	AAAGACCGCT	TTAAAGCCCT	420
TTACTGGGAT	GGTCAAGGAT	TTTGCTACT	ATATAAACGC	TTTGAGAACG	GAAAAC TGAC	480
TTGACCAAGT	ACAGAAAAGG	ATGTCAAAGC	TCTCACACCA	GAACAAGTAG	ACTGGCTTAT	540
GAAGGGCTTT	TCTATCACTC	CCCAAATATA	GTGGATT TAA	ACTAGAATAG	TACACCCCTA	600
CTTCTAAAAC	ATTGTTAGAA	ATCGATTTGA	CTGTCCTGAT	CAATTTGTCC	TGTTCTTATT	660
TCATTTTACT	ATAGAATCCA	TCTGAAAGCC	GTTTATGATT	TCTATTGAAA	TGAAGACCGT	720
CCATTTTAGT	AGACTAAAGG	ATTACTCAAA	ACTTCGAGAA	GGAAGACAGA	TGAAC TTGTT	780
TCTTATAAAA	ATGTTGTCTG	AAACTATTCTG	CTTTTTTCCA	GAAATTTTAG	AGGAAGAAAA	840
CTTTATGAGG	AAAAAGGAGT	TACTCAAATA	ACAATTCAGG	ATTAAAAATA	GACAGTTGAG	900
GAGCGGAAGG	TATAAATTAA	GTTTGCTACT	GTATAATGGA	TTTAAATCAC	TCAGCAGACA	960
GAACGAATAC	TCTTCGAAAA	TCTCTTCAAA	CCACGTCAGC	TTCGCCTTGC	CGTAGATCCA	1020

TAGGGGACTG	GACTTCATCA	GTTCTATCAA	CAACCTCAAA	ACAGTGTTC	GAGCTGACTT	1080
CGATCAATTT	TATCTGCACC	TCAAAGCTGT	ACTTTGAGCA	AGCCTGACGA	CTAGCTTCCT	1140
ATTTGATTTT	CATTGAATAT	CAGAACTCA	TTCTCCATCA	AATAATTCGA	CTGCGTCTAA	1200
TAATTTTTGG	TCTGGCACGG	TGTCAGAAAT	AAAGGTTGTG	TATTTGGAGA	GGGGATTAAT	1260
TTTAAAAAAT	CCAGTCTTGT	AAAATTTAGA	ACTATCAATC	AGTAAGATGG	TTTCATGGGC	1320
TTTGTCAATA	ATATTCTTTT	TTGAAATAG				1349

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

CTTTTTTATA	AGCAATTCAA	TTTTTACTC	ATCTGCTTTC	AAAAAGCATT	CTAGTCCATC	60
TCCGATTAA	GATGGACTTT	ATCACCTCCT	TCTCCAATCC	TTGTATGACA	TCTTGAAGTT	120
GATTCATGAC	ATCTTCCAAA	ATTTCGAAAG	CTTTATTCTT	AAATCCACGT	TTACGAATCT	180
CTTTCCACAC	TTGTTCAATG	GGGTTTCATCT	CTGGTGTGTA	TGGAGGAATA	AATGCAAAAC	240
CAATATTAGT	CGGAATCTTT	AAGACACTTG	ATTTATGCCA	TATAGCATTG	TCCATAACGA	300
GTAAAAAATA	ATCATCTGGA	TAAGCTTGTG	AAAGCTCTTC	TAAAAAGGCG	TTCATCCACT	360
CAGTATTACA	TCTACCAGCT	ATTAAGAAAA	AATGATTCCG	CCTGTTATGG	GCATCAACAG	420
CTCCATAACA	ATAGTGAAAT	TCTCGTATAT	AGTGAATATG	GACATGTGGA	CCTACTCCTA	480
TTGGAGACCA	ACAAGATCCC	AGTTTACTGA	TTCTACCGAA	ACCAGCCTCA	TCTTGGTACA	540
TCAAGCGAAC	CTTATGAAAA	CGTCTACTGG	TTTAAATCGC	TTTCTTGTCT	TCTTGAATTG	600
AGATTTTATT	TTTAGACGCG	ACAATGGTTT	GAGCGTCTGC	TTTCTTAGGA	TGTTCTGGAC	660
GTGGCATAAT	ATTTCGCCAG	CCATGGCGCT	TCAACAGTTG	ATAGAAGGCA	TCACGTGTGT	720
AGGAACGACC	TAACTCCTTT	TTATAAGCCT	GAAATAAGGC	ATCAATTGTA	ACAAATTCTC	780
CTGCCTCTGT	AGCCTTCAAA	TGGCGGGCAA	GAAATACTTT	CTCTTCCTCA	ACTGTCATAT	840
ATGCATGGTT	ACACCACCAC	TTTCCTGATA	GAGTTGTTCA	CATCTTATTT	CAAACACTA	900
TAAAAGTTCT	ATAATCTCTT	TATAAGATTT	GCCCATCAGA	CGAAATATAA	TAAATTGAAA	960
CTAGAATAGT	ACACCTCTAC	TTCTAAAACA	TTGTTAGAAA	TCGATTTGAC	TGTCCTGATC	1020
GATTTGCCCT	ATTCTTGTTT	CGTTTTACTA	TAGAACGATT	TGAAGGCGTT	TATGATATTG	1080
AGCTGTACGA	GAGTCTTTTA	AAAGTGTTTT	GATGGCTTGG	ATTTCTTCTT	TAGTTGATTT	1140
CATATCACTA	TTATATAATG	CTTTTGTATC	TTTAGTTTAG	TATTATCGTA	GAAAATGGAC	1200
TAGGTGCTAT	GGATACACCG	GATGAGAATG	GTTATGTAGC	AGATGACTAT	CGGATTACTT	1260
ACTTAGAGGC	CCACATCAAG	GCCATGCGAG	ATGCCATTTA	CCNAGACGGG	GTTGACTTGC	1320
TTGGTTATAC	GACTTGGGGC	TGTATCGATC	CAGTTTCAG			1359

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

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CTAGTATTTTC CGTTGTGNTT AGTTTGTCTG CCTATGGAGT TATTGCCTAT GTGCAAGGTC      60
AGNTGGATAT TCTTCTAGTG ATTCTGGCCA TGATTGGTGG TTTGCTCAGT TTCTTCATCT      120
TTAACCATAA GCCTGCTAAG ATCTTTATGG GTGATGTGGG AAGTTTGGCT TTAGGTGGAA      180
TGCTGGCAGC TATCTCTATG GCTCTCCACC AAGAATGGAC TCTCTTGATT ATCGGAATTG      240
TGTATGTTTT TGAAACAAC TCTGTTATGA TGCAAGTCAG TTATTTCAAA CTGACAGGTG      300
GTAAACGTAT TTTCCGTATG ACGCCTGTAC ATCACCATTT TGAGCTTGGG GGATTGTCTG      360
GTAAAGGAAA TCCTTGGAGC GAGTGAAGG TTGACTTCTT CTTTGGGGA GTTGGGCTTC      420
TAGCAAGTCT CCTGACCCTA GCAATTTTAT ATTTGATGTA AGAATGGCAC CCTGATGTTT      480
TAGGGTGTTT TTGTGTTTAA ATACACAATG AAAATCAAAG AACAACTAG AAAGCTAACT      540
TTAGGCTGCT CAAAACATAG TATATTGAAA CTAAAATAGT ACACCTCTAC TTCTAAAACA      600
TTGTTAGAAA TCGATTTGAC TGCCTGATT ACGATTTATC CTGTTCTTAT TTCATTTTAC      660
TATACCATCA ATAAGTGTTG AAAAGATCGT TGACAGAACT GACCAAGCCA GATCATCTTT      720
GTAACCACCT TGAGCTTGTA GCATATTTGT TAATTGAGCA AAGGCGCTAG AAGAGTTTGC      780
TGGGTCAGCA GTTGCGATTT TTCCTTTTAG TTCAGGTTTG AGAAGGTCGC TATATCCTTC      840
GATGTTTCATG CCTTTAGTTA AATCAGGGTG GACGATTAAA AACTACCAT CTAGTGTATA      900
AGGAGTAGAG AAGCCAGTTG TGTTTTGATA TTCTTTGATA ACATTATCAT TTTCTTTTGA      960
AATATAGTTT TCAAAGAGTT CTCCGTGGGT AGCATATTGT GTTATAAGAA CCACCAAAGA     1020
TAACATCAGC TACAGGAACT TCTTTTTCTG ACCTAGTTTT TTGAAAAGTT CTCCAGTACC     1080
AG

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(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1303 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

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CTGGACTTGA TAGGCATCTT TGTAATCCTC TAAAGCCTCT TTCATCAAGG CACTACCAAT      60

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TCCTTGACGC	TGATAGATTG	GTAAAACGAT	TAAATCCTGA	ACCAATACTG	ATGAGAATCC	120
ATCTCCAACC	AAACGAATCA	AGCCCACCAC	AGCATCACCA	TCAAGTGCCA	CATAAATTAC	180
TAATGAATGA	GATAAGGCCT	GCTCCAGCAT	CTCTGGTTGA	TGGGTATAAT	TAGTCCAACC	240
GACAGCCTGA	TAGACATGTA	AAACATCCTC	TAGCTTGACA	ATTTCTTGCT	TTTTAATAGT	300
AATCATCTCA	ACACCTCTTA	AAGTTCTCTC	AAGCTCTTGT	ACTGCTGTCC	ATTTTTATCA	360
AAATTTTCAG	GACGCAACCA	TGTTTCCAAA	CGATCTTTGA	CTTTGGGCCA	GTCTTATCA	420
ATCATAGACA	ACCAATCCAT	ATCTCTCGTA	CGCCCCTTAT	AAACCACTGC	CTGACGGAAG	480
GTTCCTTCAT	AAATAAAGCC	CAAACGCTCC	GCAGCACGTC	TGGATGGCAG	GTTAAGAGCA	540
TCGCATTTCC	ACTCATAACG	ACGATAGTTA	AGCTCTTCAA	AGACATAGCG	AGCCAGTAGA	600
TACTGGGCTT	CTGTCCCTAT	CCGTGTCCCC	CTGAGTTTTG	GAGAAAAAGT	GACAGCTCCC	660
ACTTCTATTA	CTCCGTTACT	GGTCAATACG	CATGAGAGAA	AAATTCCCAA	AGCCTTACCA	720
GTTGCCTTGT	CTATGTAGTA	AAAACGGTCC	TTACGAGCCA	ACATCTGACT	ACTATAGTAG	780
ATTGAAACTA	GAATAATATA	CCTCTACTTC	TAAAATATTG	TTAGAAATCG	ATTTGACTTC	840
CCTGATCGAT	TCGTCCTATT	CTTATTTTCAT	TTTAATATAA	TTGATAGTGG	TCGCCCCAGC	900
CAGATACCTT	ATCTGCTATC	CATTTAGGAA	CCCCTAACTT	AAGCAATCCC	CATAATCGTC	960
TCGATTTCTT	CTTCCATTGC	TTCCAGATAA	TCACTCGTAG	GCGAGTACGC	AAGCGCTCAT	1020
CTATGTTAGT	GACTATACTT	TTCATATTTA	TAATTCATTC	CTTTCGTTTC	ACTCAAGGCA	1080
CAACACAGAA	TGAAAAAGTG	TTGTGATCTT	TATTTTGTTT	TATAATAATA	GTGAGAAAGC	1140
CTATCACTAC	TACAAATCAC	GGGGAGGTGA	ATAAGTGAGT	GGTACAGCCA	CTACCTCGCA	1200
TATTTTGTC	CATCATTTAA	CGGTACATAA	TAAGTTGTAC	CATCTGAATA	AGTTGCTACA	1260
ATATCATTTG	CATGCTCTCC	TTCACCTTTA	GCAAAGGTTG	GAG		1303

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

CTCTTCAATC	AACTCACGCT	TTAGGGCTTC	CTGATGATTT	TCACCTGCTT	CAATTTCTCC	60
ACATGGTAGG	AACCAAGCAC	CATTTGGTTC	TTGAACAAGA	ACAATTTGTT	TTTGTTTCAGG	120
ATTAGGGATA	ACTGCATATA	CGCCATAGCG	AGCAATATAG	TCTGTATTTCG	CTTTTTTCTC	180
CGAAAGTTGG	GTTTGCCATT	GCATTTTCCT	CATTATCTAG	TATCGTTATT	ATTATAGTGA	240
AATGAACCAA	AAATAGTACA	CAATGTGGTA	TAATCTTTTT	ATGGCATATT	CAATAGATTT	300
TCGTAAAAAA	GTTCTCTCTT	ATTGTGAGCG	AACAGGTAGT	ATAACAGAAG	CATCACACGT	360
TTTCCAAATC	TCACGTAATA	CCATTTATGG	CTGGTTAAAG	CTAAAAGAGA	AAACAGGAGA	420
GCTAAACCAC	CAAGTAAAAG	GAACAAAACC	AAGAAAAGTT	GATAGAGATA	GACTTAAAAA	480
CTATCTTACT	GACAATCCAG	ACGCTTATTT	GAAGTAAATA	GCTTCTGAAT	TTGGCTGTCA	540
TCCAACCTACC	ATCCACTATG	CACTCAAAGC	TATGGGCTAC	ACTCGAAAAA	AAGAACCACA	600

CCTACTATGA	ACAAGACCCA	GAAAAAGTAG	CCTTATTTCT	TAAGAATTTT	ANTAGTTTAA	660
AGCACCTAGC	ACAGGTCTAA	CAAATGGTGA	ATTAATCGCT	CCAATGACTT	ACGAAGAGAT	720
GATGACGAGC	GACTTTTTTG	AAGTATGGTT	TCAGAAGTTT	CTCTTACCAA	CATTAACCAC	780
ACCATCGGTT	ATTATAGTGA	AATGAAATAA	GAACAGGACN	AATCGATCAG	GACAGTAAAA	840
TCGAATTCTA	ACAATGTTTT	AGAAGTAGAG	GTGTACTATT	CTAGTTTCAA	TCTACTATAT	900
TAATGGACAA	TGCAAGATTC	CATAGAATGG	GTAAGCTAGA	GTTCTTATGT	GAAGAGTTTG	960
GGCATAAACT	TTTACCTTTT	CCTCCCTACT	CATCTTAGTA	TAGAAAAGTG	AATCTAAAT	1020
AGTACATAAC	TGCTTCTAAA	ACATTCTTAT	AAATTGATTT	AAATTCTCAA	ATCATATTAT	1080
TCAGTTCTTA	TTTCATTTTG	CTCTACAATC	CTGTTGAGAA	GACACGTGTT	CATATCAAAA	1140
AGGTATTGGC	AAGTTGCAAT	ACCTTTTTAC	AAGGTTCTTT	TGTCTTATTT	TTGTTTCAAC	1200
TGACTATATC	TCCTATGGTT	CTAGTTCAGA	AGGCTAGGCT	ATAATTATGA	TTGATAAGAA	1260
GTATCATTCC	AAGTATTGAG	AGTGAATGTT	TCAAAATCAT	GGGTTTCTAT	AATGGTCAGG	1320
CTGGCATTTC	CTAGACCGCC	ATCTTTACGA	AGAAGTGGTT	CTTTATAGCC	TAGGAGAGTA	1380
CGAAGACTGG	CAGTAAGATT	GGCGCCGTGT	CCGACAATTA	GAATACGCTC	AGCTGGACTA	1440
TCTTTTAATG	ATTTGATAAA	TTGGATGGTC	CGCTGAGTTG	TACTATAGAG	GGATTCCGGCT	1500
CCGAACATTC	GAGTGTCAA	TTGAGCAAGA	TTTGAACGAA	AAGCCTGGAT	TTGTTGCGGG	1560
TAAATAG						1567

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

CTGTTTCCAT	AGCATGACTT	CTGTACTAGA	CTTTCTTTTC	CGAATAAATA	GATAGAACCA	60
CAGAATCTAG	TAAACCTAGA	ATTAAAATTA	TGGTATAATA	TTAGCAATAA	AAGAAATCTG	120
GAGGATTAGA	ATCATGGTAT	CAACGAAAAC	ACAAATTGCT	GGTTTTGAGT	TTGACAATTG	180
CTTGATGAAT	GCAGCAGGTG	TGGCTTGAT	GACGATAGAG	GAGTTAGAAG	AGGTCAAAAA	240
CTCAGCGGCA	GGAACCTTTG	TTACTAAGAC	AGCGACCTTG	GACTTCCGTC	AGGGGAATCC	300
TGAGCCACGC	TACCAAGATG	TTCCACTTGG	TTCCATCAAC	TCTATGGGCT	TGCCAAATAA	360
TGGCTTAGAC	TATTATTTGG	ATTATCTTTT	AGATTTGCAG	GAAAAAGAGT	CGAACCGAAC	420
TTTCTTCTTA	TCTCTGGTCG	GCATGTCTCC	AGAGAAACCC	ATACTATTTT	GAAAAAAGTC	480
CAGAGA						486

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

CTCTATCAGG AAAGTTAAAT TAATTTATAG AAATATTTTA GTATTTAAGC CCTACTGTTA	60
TAGATTCAAT ACACTATATA TGTGTTTGTC TGATAAAAAT TTCTACTCTT TTTGATTTTA	120
AATAAGTATT AGTTTACATT ATGGTGTGAA TTGGGTTTGA TATCTCTTTT GAGGAAGTTG	180
CCTTAGATTT TTCTGATTGT GTTTTATTGT ACAGTGTATC TTGCTTGTTT TGAACAGAAT	240
TTTTTATGAC ATTTGTCATA TTTTCTAGTG ACAGAAGCTT CTGCCTCCTC TGATTTTAAA	300
AGACTATAAT TGTAAGTATGA AATGGGGGAA GAAGAGATGA GAAATAAAAT GATTATCGCA	360
GTAAGTTTAG TAGTAGCAGG AGTTATGACC TATCTCATGT TTCGGGATT GGATGAGAAT	420
TTCTACCATT TTCCTTGGA GGTCTTTGCT GGCTTTGGAA TCATCTTCTT GGCTTGTC	480
GAGAAGGTTT GAAATTAGTA AGAGATGTGA AAAAGGAGTT TGA AAAAATGA AAAAAGCAAC	540
TATCTATTTT TTTATCGGCC TGTCACCTCTT GGTATGGTTG GTAGAAATGT TTACAGGTTG	600
GTTTGCTCAA ACCTTCCTTC ACCAGTTCAT CCGTGGTGCA TGGGGATTAG GATTTATGAT	660
TTTTATCGCC TTTCCGATGG GAAAGGAGTT GCTGGAAGGA GAATATCATG AACATGATTA	720
AGGTTCAAGG ACTACATAAA AATATTAAGG GCAAGGCTAT TTCAAAGGAT ATTCCTTTG	780
AAGTAGCAGA AGGTGAATGC GTTGCCCTGA TTGG	814

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

CTTGGTACGA CCGTATGGGT GGTCACGTAA AGTGGGAAAC TTCCAAGATG GGCACGTGTG	60
ACGGATCCCC GTAAACTGTC GCANAAGAAC TGAAGATGAT GTTTTTACAG TTGTTTCTT	120
CCATGGCTTT CAAAAGGCTG ACAGTTCCAG CGATATTGTT GTCATAGTAG GCAAGAGGGA	180
TACGTGTTGA TTCGCCAACA GCCTTCAAAC CAGCAAAGTG AATGACACCA GTCAGTTCTT	240
CCTGCTTGAA AATATCTCTG AGGGTATCTG TGTCACNAAT ATCTGCCTCA TAGAAAGGAA	300
TCTCAACTCC TGTGATTCTT TCAACAACCT CTAAACTCTT ACNATTGCTA TTGACAAGAT	360
TATCCACCAC AACAACTTGA TGGCCTGCTT GGATCAATTC AATAACAGTG TGGGTTCCAA	420
TAAAACCGGC ACCACCAGTT ACCAAAATCT TTTCTTGCA TTTTTCCT CGATTCTCAG	480
ATTATTTTTT CTTATTTTAA CCATTTTGA CAGGGAATGT CATTTGCCAC CTTAAACTAC	540

CTGATAAAAT	TTCAGTAAAA	TGCTTATACT	CTTGGAATAAT	CCAATTCAAA	CCACGTCAAC	600
GTCGCCTTGC	CATGGGTATG	GTTACTGACT	TCGTCAGTTC	TATCCACAAC	CTCAAAGCAG	660
CGCTTTGAGT	AACCCGCGGC	TAGTTTCNTA	GTTTGTTCCT	TGATTTTCAT	TGAGTATTAT	720
TCGCTTTTTA	CTCGTTTGAC	ATAGTTTTCA	ATTGGGTAGT	TTTCAGGGTC	CAAGGTCAAC	780
TCCTTGTCTT	GGATCAGTTG	AGCTAAATGG	TAACCAATAA	TAGGACCAGT	TGTGAGGCCT	840
GATGAACCTA	GTCCACTGGC	TGCATAGACA	CCAGTTAAGT	CAGGCACCTG	CCCAAAGAAA	900
GGAGAGAAAT	CACTGGTGTA	GGCACGGATT	CCAACACGCT	CAGATTTTGA	AGTAGCTTCA	960
GCCAAAATCA	GATAGTGAGT	CAAGGTGGCC	TCCTCCATTT	GTTGGAGCAA	GGTTTCATCT	1020
ACCGTCAAAT	CAAATCCCAT	GTCATTTTCG	TGGGTAGCGC	CTAAGGACAA	TTTCCCACCT	1080
GCAAAAGGAA	TCAAATCCCA	CTCCCCTTCT	GGCATGACAA	CAGGGTAAGC	TTCCATGTCT	1140
TGGACCAGCT	GATAATCTCG	TAGTTGTCCT	TTTTGAGGAC	GAACATCTAC	TTCATAACCC	1200
AAGGGTTCTA	ACATGTCCCC	CAACCAAGCT	CCNGTCGCCA	AAATAACCTG	CTCAAACCTC	1260
TCTTCACCAA	TCTGGTAGCC	TGATGCTAAC	GGTGTCAGAG	TCACTTTTTC	TTTGACCAG	1319

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

CTCAAATAC	TGTTTTGAGG	TTGCAGATGG	AAGCTGACGC	GGTTTAAAGA	GATTTTCGAA	60
GAGTATAAAC	TGCTTATAAA	ATAAAAAGGA	GCCCTGATGG	AACACATTAT	TTATCAGTTT	120
GAAGAGGACT	TGGCAATCCT	TACCTTGAAC	CGTCCTGAGG	TCGCAAATGG	TTTTCATATT	180
CCCATGTGTG	AGGAGATTTT	AGAAGCTCTG	ACTTTGGCAG	AAGAAAATCC	AGCTGTGCAT	240
TTTATCTTAA	TCAATGCCAA	TGGAAAGGTC	TTCTCAGTTG	GGGGAGATTT	GGTAGAGATG	300
AAGCGGGCAG	TGGATGAGGA	TGATATTCCA	TCATTGACAA	AAATCGCAGA	GTTGGTCAAT	360
ACGATTTCTT	ATAAAATCAA	GCAAATAGCC	AAACCTGTTT	TTAATGGAAG	TTGACGGTGC	420
TGTTGCAGGT	GCCGCAGCGA	ATATGGCTGT	TGCGGCAGAT	TTCTGTTTGG	CGACGGATAA	480
GGCTAAGTTT	ATCCCAAGCC	CTTTGTTGGT	GTGGTTGGCT	CCAGATTCCA	GGGG	534

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 784 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

CTGCAGCCGG	AAGTTATCTG	GTTACAAAAA	ATCGCCAAAC	CATCACAGAT	GAAAGTCTTG	60
AATACCACTG	ACCGCGTTCA	AGCTATCAAG	GACGATGTGG	ATATTATCCA	AAACAGCCTG	120
CAAATCATT	ACCAGCAAAA	AGAACTTATC	AAGGAATACC	AAGAAGACTT	GACTTACAAG	180
TTTAAGGTCT	TGGAAAAGGA	TATCCAAACT	AGGACTAGCT	GTGATAAAAG	AAATGCAGGG	240
AACTGAAGAT	AAGTAAAAAG	AGCCCCGACG	CTCTTTTTTA	AAACGTAAAC	AAGTTATAGT	300
GAATTGAATT	TAGAATAGCA	CATCATAGTT	TCTAAAGCAT	TGTTAGAGAT	TACTTTAAAA	360
TCCTCTTATC	AATTTGTTCA	TATTCTATTT	CAATCTACTA	TATATATCCC	ATCAACTATG	420
CATCATAATT	TAGGTAACCT	ATACTCAATA	AAAATCAAAA	AGCAAACCTAG	AAAGCTAGGC	480
ACAGACTGCT	CAAAACACCG	TTTTAAGGTT	GTGGATAGAA	CTGACGAAGT	CAGTAACCAT	540
ACCCATGACA	AGCCGACGCT	GACGTGGTTT	GAAGAAATTT	TTGAAGAGTA	TCATTCACCA	600
TTTCACAAC	AAATCGAAGA	CTTTCTGCCG	TAATGAAAAC	ACCTGAAACA	GCTTGGTTTC	660
AGCTGTCCGG	AAACTTTAAG	ACTTAGGTTT	AAAGTTTAGG	TATGGAACCT	CGAAGGAGGT	720
CGCTACCGTC	CGTCATTACT	TAGNGAAGNC	TTAAAAAATC	TATAAAGTAA	AAAGAGCCCC	780
ACAG						784

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 962 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

CTACTCGTTT	TAGTATAGTA	AACTGAATCT	AGACTAGCAC	AATGCNGCTT	CTANAGCGTT	60
TCGAAACTAG	AATAGGACAA	CATAACTGCT	AAAAGATTTT	TATAAATTCA	TTTGATTTTC	120
CTAATCAATT	TGTTCTGATC	CTANTTCACT	CCACTATAAA	ATATTCTTAT	CAATTGATTT	180
GNATGCCAAA	ATTCCATCGT	TCAGGTCTTA	TTTCATTNGG	CTNTAAAAAA	CTCTCCTGGG	240
NAATCCCAGG	AGAGNATGAT	TACNTATTTG	AACTTGAATC	CTTCGTANAT	AAGCTCTGTT	300
TTTGGAATTT	GTTTCTTAAT	CTGTTTGGCA	AGTGCCTTCA	TCATAGAAAT	AGGACCACAC	360
ATATAGACGG	TTGCATGTTT	GGGCACTTTT	TTTGTTCAAA	ATTAAGATAG	CCGTCTTTTC	420
TACTGTTCGAT	TAGATGGAGT	TCAAAATTAG	GATTTTTTCT	AGCATAGTTA	CGGAGTAAAT	480
CTAGGTAGAC	TGCATTTTCA	TCTCCACGGA	AGCTATAGTA	GAAGTGAACC	TGTTTATCTA	540
AAATAGGATG	TTCACGGATG	TAAGAGATGA	AGGGGGTGAT	CCCAATACCT	CCAGCAATCC	600
AAACCTGATT	TTCTCGTCCT	TCTTCTATGA	TCATGTGTCC	GTAAGCTCTG	TCTAGGGTTA	660
CTTTGCTGCC	GGCTTGAAGA	TTATCATAGA	TATTTCTTGG	TATGGTCGCC	TGAATTTTTA	720
ACAGTAAAGT	TAAAGAGTTT	GAACCCATGA	ACTCCCTGAG	AATAGAAAAG	GGATGCCGGA	780

ACCACTTTCA	AAGCCTTCTT	GGAAAATCTT	TAGAAAGGCA	AATTGTCCTG	ATTGATAGTT	840
GAAAGGTCTG	CTAAGATGGA	TTTGAATTTT	TCTAGTATCG	TGATTTAAGC	GTTTGAGATG	900
GGTAATTTTC	CCTAGATAGG	GGAAGGAAAT	CTTTTGATAT	AGAAAAATGA	TATAAAAACC	960
AG						962

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 910 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

CTCTTTCCAC	TATTATAACA	CGAAAGAAAG	AATTGTCAGG	GAAGTGTACA	GATTTCTTTT	60
CTATCTATTT	ATAACTCAAT	GAAAATCAAA	GAGCAAAC TA	GGAAACTAGC	CGCAGGCTGT	120
AATTGAGTAC	GGCAAGGCGA	CGTTGACGCG	ATTTGAATTT	GATTTTCGCA	GAGTATTATT	180
CGTAAAAAAT	CTCAAAAAGC	CTACCTTTTCG	G TAGACTTAG	TTTGTTTCTA	TTCTAATCGG	240
CACTCTTCCA	AAATTTTGCT	CTGCTATACT	TGGCTTTCCCT	AGTTGGTAAA	TCTGGTCAAC	300
CTTTTGAGTC	ATAGCATCCC	AAGGTTCTTT	GCCAATTTCGG	CTGACTAGAT	TGACCTGTCC	360
TTTCAGAGAC	TTGAGATGTT	GCCTGCCTTT	TTCAGTAAAT	CCAAGGACAT	GAATGGCTTC	420
TGGCAAGTCA	CTTTCTCTAG	CCTGCATCAA	AATATAGGTC	AATAGGCGTC	TGACACGCGC	480
CTTGGTGTA	CGTTTGGTAG	TCACTAACTC	GACCAATTCT	TCCACAGACT	GGGCTGTTTT	540
AATAGCTTCT	TTAATGCGCA	CAGCCATTTT	TTGATTGACC	TGATAGATGG	TGGTTAGGTC	600
GGGATTTGAC	AAGATTTGAT	AGCGGAGCAA	GGGAAAATAG	TCTTCCCAGA	TCACCTTACT	660
GGCTTGCTCA	AATAGGGCAA	CAGAAGGCAT	AAAACGTTCT	AAGAAATCTT	GGTCCTTCTG	720
ATGTTGACGG	AGGGCTGTCT	CCGAGGCAAA	GTCCACATCT	TTATTCACAG	AATGGTAACC	780
TGCCCCCTGA	CGCTGAATCG	GATGCAGCTT	GATATTCCGT	CCTGCAACCG	CCTTGGCATA	840
GGCCAAAACA	AAGAACATGA	TTGGGGTGTA	TTACCTGAAA	AATCAAGACC	AGCAAATTCC	900
TTCCACATAG						910

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 866 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

CGCCAAGTCA	TCCAACAAGT	CCAGAACGGT	TCTGGGGCTT	GGGATCCTCA	GTCGCTGGAG	60
ATAACTCCTT	TGGGCTTGTT	CATCATGTAG	TAGACAAACT	CTTCATACTC	CAACACTTGC	120
CCATCAAAAG	CGAATCTCAT	CTATTTTTTC	ATCAATCTGC	AATTTAGCTG	ATTTTTCTTT	180
TTTACCATTT	ACAGTCACGC	GCCCAGCCTT	GAGCAAGTTT	TTGACCTCAG	TCCGACTTCC	240
CACCGCACAG	GCAACTAAAA	ATTTATCTAA	TCTCATAGAA	CTATTATATC	ATATCAAAAG	300
GAGGCTGGTA	CAATGACCAA	CCTCCTTTTC	GTTTCATACT	CTTCAAAAAT	CTCTTCAAAC	360
CGCGTCAACG	TCGCCTTGCC	GTATATATGT	TACTGACTTC	GTCAGTTCTA	TCTGCAACCT	420
CAAAGCAGTG	CTTTGAGCAA	CCTGCGGCTA	GTTTCCTAGT	TTGCTCTTTG	ATTTTCATTG	480
AGTATCAGAT	TTAGGAAATT	AACTTCCTCG	TCTCCAAAAA	ATAGCTAAGA	CAATCATGGC	540
ACCTAAAACA	GCTGGGATAA	TAGCTGTTCC	TGATAAAACT	GGCCCCCAAG	TTCCAAAGAG	600
CAAGTGACCT	AGAAAGGCTC	CGATCCAACC	GAGAAACATT	TTTCCAAAAC	ATCCCATTCTG	660
CTCTCCACGA	TTGGTCATAG	CACCTGCTAA	AAATCCCCT	AGGAGACCAA	CGAACATACT	720
TCCTAACATA	TTATCTCCTT	AATTTGCCCA	ATTCCCATT	CGGAAAAGAA	GTAATCGCGT	780
TCCATCCTCA	CGAATACCAT	CGATATCCAT	TTGGTTAGAA	CCAATCATAA	AGTATACGTG	840
AACATCTGAA	CGGTTAAGCC	CTGCAG				866

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

CTTCAGGATG	TGGGAAAACG	ACCCTTCTTC	GTATGATTGC	AGGTTTCAAC	AGTATCAAAG	60
ATGGAGAATT	TTACTTCGAT	GATACAAAAA	TCAATAATAT	GGAACCCAGC	AAACGCAATA	120
TCGGGCTGGT	TTTCCAAAAC	TACGCTATTT	TCCCACATTT	GACTGTCCGA	GACAACGTTG	180
CTTTTGGTCT	TATGCAAAAG	AAGGTTCCAA	AAGAAGAATT	GATTCAACAG	ACCAACAAGT	240
ATCTTGGAAT	CATGCAAAAT	GCTCAATATG	CGGATCGAAA	GCCCGATAAA	CTCAGTGGTG	300
GACAACAACA	ACGTGTCACC	TTGGCATGCG	TCTTAGCGGT	TAATCCAAGT	GTTCTCCTCC	360
ATGGACGAAG	CCACTTAGTA	ATCTGGAGGC	CAAACCTTCG	TTGGATATGC	GTTCAAGCCC	420
ATCCCGAGAA	ATCCAACCAC	GAAGTTGGGG	AATTACAAC	GTTTATGTAA	CCCACGACCA	480
AGAAGGAGCC	ATGGCTATTT	CAGACCAAAT	TGCCTGTTAT	GAAAGATGGG	GTGATCCAAC	540
AAATCGGCCG	ACCAAAAGAA	CTGTATCATA	AACCAGCTAA	TGAGTTAGTG	GCAACCTTTA	600
TCGGACGCAC	AAATATTATC	CCTGCCAATC	TTGAAAAACG	GAGCGACGGC	GNTTATATCG	660
TCTNTTCAGA	TGGANANGCC	CTTCGAATGA	TAG			693

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

```

Met Ser Met Phe Thr Met Val Lys Met Asn Pro Leu Arg Gly Leu Ile
 1             5             10             15
Cys Asn Leu Lys Gly Asn Lys Ile Thr Ala Leu Ile Gly Pro Ser Gly
          20             25             30
Ser Gly Lys Ser Thr Tyr Leu Arg Ser Leu Asn Arg Met Asn Asp Thr
          35             40             45
Ile Asp Ile Ala Lys Val Thr Gly Gln Ile Leu Tyr Arg Gly Ile Asp
          50             55             60
Val Asn Arg Pro Glu Ile Asn Val Tyr Glu Met Arg Lys His Ile Gly
65             70             75             80
Met Val Phe Gln Arg Pro Asn Pro Phe Ala Lys Ser Ile Tyr Arg Asn
          85             90             95
Ile Thr Phe Ala His Glu Arg Ala Gly Val Lys Asp Lys Gln Val Leu
          100            105            110
Asp Glu Ile Val Glu Thr Ser Leu Ser Gln Ala Ala Leu Trp Asp Gln
          115            120            125
Val Lys Asp Asp Leu His Lys Ser Ala Leu Thr Leu Ser Gly Gly Gln
          130            135            140
Gln Gln Arg Leu Cys Ile Ala Arg Ala Ile Ser Val Lys Pro Asp Ile
145            150            155            160
Leu Leu Met Asp Glu Pro Ser Leu Ser Leu Gly Ser Asp Cys Asp His
          165            170            175
Ala Thr Arg Arg Asp His Val
          180

```

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

```

Met Ile Lys Ile Ser Asn Leu Ser Lys Ser Phe Ser Gly Gln Thr Val
 1             5             10             15
Leu Asp His Leu Asn Leu Asp Ile Gln Lys Gly Glu Val Val Ala Leu
      20             25             30
Ile Gly Ser Ser Gly Ala Gly Lys Ser Thr Phe Leu Arg Ser Leu Asn
      35             40             45
Tyr Leu Glu Thr Pro Asp Ser Gly Ser Ile Gln Ile Asp Gly Phe Ser
      50             55             60
Val Asp Phe Ser Lys Ile Thr Gln Glu Glu Ile Leu Ala Leu Arg Arg
      65             70             75             80
Lys Leu Ser Met Val Phe Gln Gln Phe Asn Leu Phe Glu Arg Arg Thr
      85             90             95
Ala Leu Asp Asn Val Lys Glu Gly Leu Val Val Val Lys Lys Leu Ser
      100            105            110
Asp Gln Glu Ala Thr Lys Ile Ala Lys Glu Glu Leu Ala Lys Val Gly
      115            120            125
Leu Ser Asp Arg Glu Asn His Tyr Pro Arg His Leu Ser Gly Gly Gln
      130            135            140
Lys Gln Arg Val Ala Leu Ala Arg Ala Leu Ala Met Lys Pro Asp Val
      145            150            155            160
Leu Leu Leu Asp Glu Pro Thr Ser Ala Leu Asp Pro Glu Leu Val Gly
      165            170            175
Glu Val Glu Lys Ser Ile Ala Asp Ala Ala Lys Ser Gly Gln Thr Met
      180            185            190
Ile Leu Val Ser His Asp Met Pro Phe Val Ala Gln Val Ala Asp Lys
      195            200            205
Ile Leu Phe Leu Asp Lys Gly Lys Ile Ile Glu Ser Gly Thr Pro Asp
      210            215            220
Glu Ile Ile His Thr Pro Lys Glu Glu Arg Thr Lys Glu Phe Phe Thr
      225            230            235            240
Ser Tyr Lys Arg Thr Tyr Ile
      245

```

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

```

Met Phe Ser Leu Arg Ser Val Phe Asp Gly Ile Pro Arg Ile Val Gln
 1             5             10             15
Gln Leu Pro Thr Thr Ile Met Leu Thr Ile Gly Gly Ala Leu Phe Gly
          20             25             30
Leu Val Leu Ala Leu Leu Phe Ala Ile Val Lys Ile Asn Arg Val Lys
      35             40             45
Ile Leu Tyr Pro Leu Gln Ala Phe Phe Val Ser Phe Leu Lys Gly Thr
      50             55             60
Pro Ile Leu Val Gln Leu Met Leu Thr Tyr Tyr Gly Ile Pro Leu Ala
65             70             75             80
Leu Lys Ala Leu Asn Gln Gln Trp Gly Thr Gly Leu Asn Ile Asn Ala
          85             90             95
Ile Pro Ala Ala Ala Phe Ala Ile Val Ala Phe Ala Phe Asn Glu Ala
          100             105             110
Ala Tyr Ala Ser Glu Thr Ile Arg Ala Ala Ile Leu Ser Val Asn Pro
          115             120             125
Gly Glu Ile Glu Ala Ala Arg Ser Leu Gly Met Thr Arg Ala Gln Val
      130             135             140
Tyr Arg Arg Val Ile Ile Pro Asn Ala Ala Val Val Ala Thr Pro Thr
145             150             155             160
Leu Ile Asn Ser Leu Ile Gly Leu Thr Lys Gly Thr Ser Leu Ala Phe
          165             170             175
Ser Ala Gly Val Val Glu Val Phe Ala Gln Ala Gln Ile Leu Gly Gly
          180             185             190
Ala Asp Tyr Arg Tyr Phe Glu Arg Phe Ile Ser Val Ala Leu Val Tyr
          195             200             205
Trp Val Val Asn Ile Gly Ile Glu Ser Leu Gly Arg Phe Ile Glu Arg
      210             215             220
Lys Met Ala Ile Ser Ala Pro Asp Thr Val Gln Thr Asp Val Lys Gly
225             230             235             240
Asp Leu Arg

```

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

```

Met Tyr Arg Ile Asp Asp Asp Glu Gln Phe Val Leu Asp Phe Leu Lys
 1             5             10             15
Gln Glu Lys Val Leu Leu Val His Gly Arg Gly Phe Asn Trp Gln Glu
          20             25             30
Pro Asp His Phe Arg Ile Val Tyr Leu Pro Arg Val Asp Glu Leu Ala
      35             40             45
Gln Ile Gln Glu Lys Met Thr Arg Phe Leu Lys Gln Tyr Arg Arg
 50             55             60

```

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

```

Met Asn Asp Glu Ala Ser Lys Gln Leu Thr Asp Ala Arg Phe Lys Arg
 1             5             10             15
Leu Val Gly Val Gln Arg Thr Thr Phe Glu Glu Ile Leu Ala Val Leu
          20             25             30
Lys Thr Ala Tyr Gln Leu Lys His Ala Lys Gly Gly Arg Lys Pro Lys
      35             40             45
Leu Ser Leu Glu Asp Leu Leu Met Ala Thr Leu Gln Tyr Val Arg Glu
 50             55             60
Tyr Arg Thr Tyr Glu Gln Ile Ala Ala Asp Phe Gly Ile His Glu Ser
 65             70             75             80
Asn Leu Ile Arg Arg Ser Gln Trp Val Glu Val Thr Leu Val Gln Ser
          85             90             95
Gly Val Thr Ile Ser Arg Thr Pro Leu Ser Ser Glu Asp Thr Val Met
          100             105             110
Ile Asp Ala Thr Glu Val Gln Ile Asn Arg Pro Lys Lys Arg Ile Ser
      115             120             125

```

Glu Ser Phe Trp
130

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

Met	Arg	Arg	Lys	Tyr	Lys	Ser	Ile	Ala	Leu	Lys	Lys	Glu	Leu	Ala	Asn	1	5	10	15
His	Ser	Gly	Lys	Lys	Lys	Phe	His	Ala	Met	Lys	Ala	Gln	Ala	Ile	Val	20	25	30	
Thr	Ser	Gln	Gly	Arg	Ile	Val	Ser	Leu	Asp	Ile	Ala	Val	Asn	Tyr	Ser	35	40	45	
His	Asp	Met	Lys	Leu	Phe	Lys	Met	Ser	Cys	Arg	Asn	Ile	Gly	Gln	Ala	50	55	60	
Gly	Lys	Ile	Leu	Ala	Asp	Ser	Gly	Tyr	Gln	Gly	Pro	Met	Lys	Ile	Tyr	65	70	75	80
Pro	Gln	Ala	Gln	Thr	Pro	Arg	Lys	Ser	Ser	Lys	Leu	Lys	Pro	Leu	Ile	85	90	95	
Ala	Glu	Asp	Lys	Ala	Tyr	Asn	His	Ala	Leu	Ser	Lys	Glu	Arg	Ser	Lys	100	105	110	
Val	Glu	Asn	Ile	Phe	Ala	Lys	Val	Lys	Thr	Phe	Lys	Met	Phe	Ser	Thr	115	120	125	
Thr	Tyr	Arg	Asn	His	Arg	Lys	Arg	Phe	Gly	Leu	Arg	Met	Asn	Leu	Ile	130	135	140	
Ala	Gly	Ile	Ile	Asn	Tyr	Glu	Leu	Gly	Phe							145	150		

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

```

Met Val Ser Ser Ser Gly Ser Glu Phe Gln Ser Gly Trp Gln Glu His
 1             5             10             15
Gln Leu Ile Ala Glu Lys Val Ser Lys Thr Leu Asp Lys Thr Phe Asp
      20             25             30
Lys Asp Val Arg Lys Ile Pro Thr Ser Pro Val Leu Ser Lys Ile Cys
      35             40             45
Arg

```

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

```

Met Ile Lys Ile Leu Ala Ala Cys Gly Ala Gly Val Asn Ser Ser His
 1             5             10             15
Gln Ile Lys Ser Ala Leu Glu Glu Glu Leu Ser Asn Arg Gly Tyr Asp
      20             25             30
Val His Cys Asp Ala Val Met Val Lys Asp Val Asn Glu Asp Leu Met
      35             40             45
Lys Gly Tyr Asp Ile Phe Thr Pro Ile Ala Ala Thr Asp Leu Gly Phe
      50             55             60
Glu Pro Gly Ile Pro Val Ile Glu Ala Gly Pro Ile Leu Phe Arg Ile
      65             70             75             80
Pro Ala Met Ser Ala Pro Val Phe Asp Asn Ile Arg Leu Pro Ala Lys
      85             90             95
Gln Asn Met Val
      100

```

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

```

Met Asn Thr Lys Met Met Ser Gln Phe Ser Val Met Asp Asn Glu Met
 1             5             10             15
Leu Ala Cys Val Glu Gly Gly Asp Ile Asp Trp Gly Arg Glu Ile Ser
      20             25             30
Cys Ala Ala Gly Val Ala Tyr Gly Ala Ile Asp Gly Cys Ala Thr Thr
      35             40             45
Val

```

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

```

Met Arg Glu Lys Glu Ile Phe Asp Ser Ile Val Thr Ile Ile Gln Glu
 1             5             10             15
Arg Gln Gly Glu Asp Phe Val Val Thr Glu Ser Leu Ser Leu Lys Asp
      20             25             30
Asp Leu Asp Ala Asp Ser Val Asp Leu Met Glu Phe Ile Leu Thr Leu
      35             40             45
Glu Asp Glu Phe Ser Ile Glu Ile Ser Asp Glu Glu Ile Asp Gln Leu
      50             55             60
Gln Ser Val Gly Asp Val Val Lys Ile Ile Gln Gly Lys
      65             70             75

```

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

```

Met Ala His Gly Asp Leu Leu Tyr His Asp Gly Leu Phe Phe Ser Ala
 1           5           10           15
Lys Lys Glu Asp Gly Thr Tyr Asp Phe His Glu Asn Phe Glu Tyr Val
          20           25           30
Thr Pro Trp Leu Lys Gln Val Asp
          35           40

```

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

```

Met Ser Leu Ile Thr His Arg Arg Phe Ile Ser Cys Asn Glu Asn Ile
 1           5           10           15
Lys His Tyr Lys Arg Leu Ile Asp Lys Ala Glu Lys Cys Val Asn Asp
          20           25           30
Leu Met Ala Glu Leu Asn Ser Val Ile Thr Thr Val Thr Gly Ile Glu
          35           40           45
Asn Arg Leu Gly Ala Val Ile Leu Ala Glu Ile Arg Asn Ile His Ala
          50           55           60
Phe Asp Asn Pro Ala Gln Leu Gln Ala Phe Ala Gly Leu Asp Ser Ser
          65           70           75           80
Ile Tyr Gln Ser Gly Gln Ile Asp Leu Val Gly Arg Met Val Lys Arg
          85           90           95
Gly Ser Leu His Leu Arg
          100

```

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

```

Met Ile Arg Ala Val Phe Phe Ser Ile Asp Asn Asp Met Glu Glu Ala
 1             5             10             15
Ala Arg Ser Met Gly Ala Ser Ser Phe Tyr Thr Met Val Arg Val Ile
          20             25             30
Ile Pro Tyr Ile Leu Pro Val Val Leu Ser Val Val Val Leu Asn Phe
          35             40             45
Asn Ser Leu Leu Ser Asp Tyr Asp Leu Ser Val Phe Leu Tyr His Pro
          50             55             60
Leu Phe Gln Pro Leu Gly Ile Val Ile Lys Gln Ser Thr Asp Glu Thr
65             70             75             80
Ala Thr Leu Asn Ala Gln Ala Met Met Phe Val Tyr Ser Val Ile Leu
          85             90             95
Met Ile Met Ser Ser Ala Ala Leu Tyr Leu Ser Ser Leu Phe Gln Gly
          100             105             110
Lys Arg Gly Lys Arg
          115

```

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

```

Met Glu Lys Cys Tyr Thr Asp Val Thr Glu Phe Ala Ile Pro Ala Ser
 1             5             10             15
Thr Gln Lys Leu Tyr Leu Ser Pro Val Leu Asp Gly Phe Asn Ser Glu
          20             25             30

```


Ile Ile Ala Tyr Asn Leu Ser Thr Ser Pro Asn Leu Glu Gln Val Gln
 35 40 45
 Thr Met Leu Glu Gln Ala Phe Thr Glu Lys His Tyr Glu Asn Thr Ile
 50 55 60
 Leu His Ser Asp Gln Gly Trp Gln Tyr Gln His Asp Ser Tyr His Arg
 65 70 75 80
 Phe Leu Arg Val Arg Glu Phe Lys His Leu Cys His Ala Arg Glu Thr
 85 90 95
 Ala Lys Thr Thr Val
 100

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

Met Glu Ile Leu Thr Thr Gln Gln Val Arg Glu Gly Tyr Gln Ala Ile
 1 5 10 15
 Leu Ala Ser Pro Leu Gly Leu Gln Asp Ala Phe Glu Val Ala Gln Glu
 20 25 30
 Lys Ser Gly Ser Tyr Thr Val Pro Pro Glu Ile Asp Gly Trp Lys Gly
 35 40 45
 Asn Thr Glu Pro Leu Arg Ile Asp Tyr Val Phe Thr Thr Lys Glu Leu
 50 55 60
 Ala Val Glu Asn Leu His Val Val Phe Asp Gly Asn Lys Ser Pro Gln
 65 70 75 80
 Val Ser Asp His Tyr Gly Leu Asn Ala Met Leu Asn Trp Lys
 85 90

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

```

Met Leu Lys His Leu Asn Leu Lys Gly His Leu Leu Thr Ala Ile Ser
 1             5             10             15
Tyr Met Ile Pro Ile Val Cys Gly Ala Gly Phe Leu Val Ala Ile Gly
      20             25             30
Leu Ala Met Gly Gly Gly Val Pro Asp Ala Leu Val Ala Gly Lys Phe
      35             40             45
Thr Ile Trp Asp Ala Leu Ala Thr Met Gly Gly Lys Ala Leu Gly Leu
      50             55             60
Leu Pro Val Val Ile Ala Thr Gly Leu Ser Tyr Ser Ile Ala Gly Lys
      65             70             75             80
Pro Gly Ile Ala Pro Gly Phe Val Val Gly Leu Ile Ala Asn Ser Val
      85             90             95
Gly Ser Gly Phe Ile Gly Gly Ile Leu Gly Gly Tyr Ile Val Gly Phe
      100            105            110
Leu Val Gln Ala Ile Ile Lys Lys Val Lys Val Pro Asn Trp Ile Lys
      115            120            125
Gly Leu Met Pro Thr Leu Ile Ile Pro Phe Val Pro Leu Trp
      130            135            140

```

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

```

Met Ile Ala Leu Gly Trp Ser Asn Ile Gly Ala Ala Ile Ala Pro Asp
 1             5             10             15
Ala Ala Leu Ala Ser Val Ala Ala Ala Ile Ile Met Val Leu Gly Gly
      20             25             30
Asp Phe Thr Lys Thr Gly Ile Gly Val Ala Gln Ala Val Ala Ile Pro
      35             40             45
Leu Ala Val Ala Gly Leu Phe Leu Thr Met Ile Val Arg Thr Ile Ser
      50             55             60

```

```

Val Gly Leu Val His Thr Ala Asp Ala Ala Ala Lys Lys Gly Asp Phe
65                               70                               75                               80
Gly Ala Val Glu Arg Ala His Phe Ile Ala Leu Leu Phe Gln Gly Leu
                               85                               90                               95
Arg Ile Ala Leu Pro Ala Ala Leu Leu Leu Met Val Pro Thr Glu Thr
                               100                              105                              110
Val Gln Ser Ile Leu Ser Ala Met Pro Asp Trp Leu Lys Asp Gly Met
                               115                              120                              125
Ala Ile Gly Gly Gly Met Val Val Ala Val Gly Tyr Ala Met Val Ile
                               130                              135                              140
Asn Met Met Ala Thr Arg Glu Val Trp Pro Phe Phe Ala Leu Gly Phe
145                               150                               155                               160
Val Leu Ala Ala Val Ser Asp Ile Thr Leu Ile Gly Phe Gly Ala Ile
                               165                               170                               175
Gly Val Ala Ile Ala Leu Ile Tyr Leu His Leu Ser Lys Thr Gly Gly
                               180                              185                              190
Asn Gly Gly Gly Gly Ala Ala Thr Ser Asn Asp Pro Ile Gly Asp Ile
                               195                              200                              205
Leu Glu Asp Tyr
                               210

```

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

```

Met Leu Asp Val Glu Ala Ile Arg Lys Asp Phe Pro Ile Leu Asp Gln
1                               5                               10                               15
Ile Val Asn Asp Glu Pro Leu Val Tyr Leu Asp Asn Ala Ala Thr Thr
                               20                               25                               30
Gln Lys Pro Leu Val Val Leu Lys Ala Ile Asn Ser Tyr Tyr Glu Gln
                               35                               40                               45
Asp Asn Ala Asn Val His Arg Gly Val His Thr Leu Ala Glu Arg Ala
                               50                               55                               60
Thr Ala Ser Leu
65

```

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

```

Met Thr Lys Leu Leu Asn Lys Lys Trp Lys Val Lys Ile Met Lys Gln
 1             5             10             15
Ile Leu Leu Val Cys Asn Ala Gly Met Ser Thr Ser Met Leu Val Lys
      20             25             30
Lys Met Gln Gln Ser Ala Thr Glu Arg Gly Ile Glu Ile Ser Ile Gln
      35             40             45
Ala Lys Ser Met Thr Glu Ala Lys Lys Asn Ile His Glu Ala Asp Val
      50             55             60
Ile Leu Ile Gly Pro Gln Ile Arg Tyr Glu Leu Leu Ala Val Lys Glu
65             70             75             80
Ile Ala Gly Asn Ile Pro Val Asp Thr Ile Asp Met Arg Asp Tyr Gly
      85             90             95
Met Met Asn Gly Ala Lys Val Leu Glu Gln Ala Leu Glu Trp Ile Gly
      100            105            110
Glu Ile Arg
      115

```

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

```

Met Val Leu Met Gln Lys Met His Gly Lys Glu Leu Ile Thr Leu Asn
 1             5             10             15

```

Gln Thr Val Lys Trp Tyr Lys Val Ser Gly Phe Met Ile Leu Leu Thr
 20 25 30
 Lys Pro Trp Tyr Tyr Leu Lys Ser Asp Gly Ser Tyr Ala Arg Asn Ala
 35 40 45
 Trp Gln Gly Asn Tyr Tyr Leu Lys Ser Asp Gly Lys Met Ala Val Asn
 50 55 60
 Glu Trp Val Tyr Asp Ala Thr Tyr Gln Ala Trp Tyr Tyr Leu Thr Ser
 65 70 75 80
 Asp Gly Ser Tyr Ala Tyr Ser Thr Trp Gln Gly Asn Tyr Tyr Pro Lys
 85 90 95
 Ile Gly Trp

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Met Leu Thr Val His Gly Lys Glu Ile Thr Ile Leu Lys Ser Asp Gly
 1 5 10 15
 Lys Met Ala Val Asn Glu Trp Val Asp Gly Gly Arg Tyr Tyr Val Gly
 20 25 30
 Ala Asp Gly Val Trp Lys Glu Gly Gln Ala Ser Thr Ala Ser Pro Ser
 35 40 45
 Asn Asp Ser Asn Ser Glu Tyr Ser Cys Cys Phe Arg Lys Gly Lys Lys
 50 55 60
 Leu
 65

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

```

Met Asn Asn Asn Phe Asn Asn Phe Asn Asn Met Asp Asp Leu Phe Asn
 1             5             10             15
Gln Leu Met Gly Gly Met Arg Gly Tyr Ser Ser Glu Asn Arg Arg Tyr
      20             25             30
Leu Ile Asn Gly Arg Glu Val Thr Pro Glu Glu Phe Ala His Tyr Arg
      35             40             45
Thr Thr Gly Gln Leu Pro Gly Asn Ala Glu Thr Asp Val Gln Met Pro
      50             55             60
Gln Gln Ala Ser Gly Met Lys Gln Asp Gly Val Leu Ala Lys Leu Gly
65             70             75             80
Arg Asn Leu Thr Ala Glu Ala Arg Glu Gly Lys Leu Asp Pro Val Ile
      85             90             95
Gly Arg Asn Lys Glu Ile Gln Glu Thr Ser Glu Ile Leu Ser Arg Arg
      100            105            110
Thr Lys Asn Asn Pro Val Leu Val Gly Asp Ala Gly Val Gly Lys Thr
      115            120            125
Ala Val Val Glu Gly Leu Ala Gln Ala Ile Val Asn Gly Asp Val Pro
      130            135            140
Ala Ala Ile Lys Asn Lys Glu Ile Ile Ser Ile Asp Ile Ser Gly Leu
145            150            155            160
Glu Ala Gly Thr Gln Tyr Arg Gly Ser Phe Glu Glu Asn Val Gln Asn
      165            170            175
Leu Val Asn Glu Val Lys Glu Ala Gly Asn Ile Ile Leu Phe Phe Asp
      180            185            190
Glu Ile His Gln Ile Leu Gly Ala Gly Ser Thr Cys Gly Asp Ser Gly
      195            200            205
Ser Lys Gly Leu Ala Asp Ile Leu Ser Gln Ser Ile Ser Leu Val Glu
      210            215            220
Asn
225

```

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

```

Met Thr Ile Phe Pro Asp Asp Phe Leu Trp Gly Gly Ala Val Ala Ala
 1           5           10           15
Asn Gln Val Glu Gly Ala Tyr Asn Glu Asp Gly Lys Gly Leu Ser Val
          20           25           30
Gln Asp Val Leu Pro Lys Gly Gly Leu Gly Glu Ala Thr Glu Asn Pro
          35           40           45
Thr Glu Asp Asn Leu Lys Leu Ile Gly Ile Asp Phe Tyr His Lys Tyr
          50           55           60
Lys Glu Asp Ile Ser Leu Phe Ser Glu Met Gly Phe Asn Val Phe Arg
65           70           75           80
Thr Ser Ile Ala Trp Ser Arg Ile Phe Pro Lys Gly Asp Glu Glu Glu
          85           90           95
Pro Asn Glu Ala Gly Leu Lys Tyr Tyr Asp Glu Leu Phe Asp Glu Leu
          100          105          110
His Ala His Gly Ile Glu Pro Leu Val Thr Leu Ser His Tyr Glu Thr
          115          120          125
Pro Leu Tyr Leu Ala Arg Lys Tyr His Gly Trp Ile Asp Arg Lys Asn
          130          135          140
Asp Ser Phe Leu
145

```

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

```

Met Ile Glu Tyr Lys Asn Val Ala Leu Arg Tyr Thr Glu Lys Asp Val
 1           5           10           15
Leu Arg Asp Val Asn Leu Gln Ile Glu Asp Gly Glu Phe Met Val Leu
          20           25           30
Val Gly Pro Ser Gly Ser Gly Lys Thr Thr Met Leu Lys Met Ile Asn
          35           40           45
Arg Leu Leu Glu Pro Thr Asp Gly Asn Ile Tyr Met Asp Gly Lys Arg
          50           55           60

```

```

Ile Lys Asp Tyr Asp Glu Arg Glu Leu Arg Leu Ser Thr Gly Tyr Val
65              70              75              80
Leu Gln Ala Ile Ala Leu Phe Pro Asn Leu Thr Val Ala Glu Asn Ile
            85              90              95
Ala Leu Ile Pro Glu Met Lys Gly Trp Ser Lys Glu Glu Ile Thr Lys
            100             105             110
Lys Thr Glu Glu Leu Leu Ala Lys Val Gly Leu Pro Val Ala Glu Tyr
            115             120             125
Gly His Arg Leu Pro Ser Glu Leu Ser Gly Gly Glu Gln Gln Arg Val
            130             135             140
Gly Ile Val Arg Ala Met Ile Gly Gln Pro Lys Ile Phe Leu Met Asp
145             150             155             160
Glu Pro Phe Ser Ala Leu Asp Ala Ile Ser Arg Lys Gln Leu Gln Val
            165             170             175
Leu Thr Lys Glu Leu His Lys Glu Phe Gly Met Thr Thr Ile Phe Val
            180             185             190
Thr His Asp Thr Asp Glu Ala Leu Lys Leu Ala Asp Arg Ile Ala Val
            195             200             205
Leu Gln Asp Gly Glu Ile Arg Gln Val Ala Asn Pro Glu Thr Ile Leu
            210             215             220
Lys Val Pro Ala Thr Asp Phe Val Ala Asp Leu Phe Gly Gly Ser Val
225             230             235             240
His Asp

```

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

```

Met Pro Phe Val Pro Gly Ile Ala Leu Thr Asn Ala Val Arg Asp Ile
1              5              10              15
Met Thr Asn His Ile Asn Ser Gly Met Ser Lys Met Phe Glu Ser Leu
            20              25              30
Leu Ile Thr Leu Ala Leu Gly Ala Gly Thr Ser Val Ala Leu Val Leu
            35              40              45

```


Met Asn

50

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

```

Met Tyr Thr Ile Arg Met Leu Lys Met Gly Ser Glu Ala Ala Ala Lys
 1             5             10             15
Ser Ala Gln Glu His Gly Leu Lys Ser Val Glu Val Thr Val Lys Gly
          20             25             30
Pro Gly Ser Gly Arg Glu Ser Ala Ile Ser Cys Ala Cys Cys Arg Trp
      35             40             45
Ser

```

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

```

Met Ile Glu Phe Glu Lys Pro Asn Ile Thr Lys Ile Asp Glu Asn Lys
 1             5             10             15
Asp Tyr Gly Lys Leu Val Ile Glu Pro Leu Glu Arg Gly Tyr Gly Thr
          20             25             30
Ala Leu Gly Asn Ser Leu Arg Arg Val Leu Leu Ala Ser Leu Pro Gly
      35             40             45
Ala Ala Val Thr Ser Ile Asn Ile Asp Gly Val Leu His Glu Phe Asp
      50             55             60

```

```

Thr Val Pro Gly Val Arg Glu Asp Val Met Gln Ile Ile Leu Asn Ile
65              70              75              80
Lys Gly Ile Ala Val Lys Ser Tyr Val Glu Asp Glu Lys Ile Ile Glu
85              90              95
Leu Asp Val Glu Gly Pro Ala Glu Val Thr Ala Gly Asp Ile Leu Thr
100            105            110
Asp Ser Asp Ile Glu Ile Val Asn Pro Asp His Tyr Leu Phe Thr Ile
115            120            125
Gly Glu Gly Ser Ser Leu Lys Ala Thr Met Thr Val Asn Ser Gly Arg
130            135            140
Gly Tyr Val Pro Ala Asp Glu Asn Lys Lys Asp Asn Ala Pro Val Gly
145            150            155            160
Thr Leu Ala Val Asp Ser Ile Tyr Thr Pro Val Thr Lys Val Asn Tyr
165            170            175
Gln Val Glu Pro Ala Arg Val Gly Ser Asn Asp Gly Phe Asp Lys Leu
180            185            190
Thr Leu Glu Ile Leu Thr Asn Gly Thr Ile Ile Pro Glu Asp Ala Leu
195            200            205
Gly Leu Ser Ala Arg Ile Leu Thr Glu His Leu Asp Leu Phe Thr Asn
210            215            220
Leu Thr Glu Ile Ala Lys Ser Thr Glu Val Met Lys Glu Ala Asp Thr
225            230            235            240
Glu Ser Asp Asp Arg Ile Leu Asp Arg Thr Ile Glu Glu Leu Asp Leu
245            250            255
Ser Val Arg Ser Tyr Asn Cys Leu Lys Arg Ala Gly Ile Asn Thr Val
260            265            270
His Asp Leu Thr Glu Lys Ser Glu Ala Glu Met Met Lys Val Arg Asn
275            280            285
Leu Gly Arg Lys Ser Leu Glu Glu Val Lys Leu Lys Leu Ile Asp Leu
290            295            300
Gly Leu Gly Leu Lys Asp Lys
305            310

```

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

```

Met Asp Ile Glu Lys Gln Arg Gly Ile Ser Val Thr Ser Ser Val Met
 1              5              10              15
Gln Phe Asp Tyr Asp Gly Lys Arg Val Asn Ile Leu Asp Thr Pro Gly
      20              25              30
His Glu Asp Phe Ser Glu Asp Thr Tyr Arg Thr Leu Met Ala Val Asp
      35              40              45
Ala Ala Val Met Val Val Asp Ser Ala Lys Gly Ile Glu Ala Gln Thr
      50              55              60
Lys Lys Leu Phe Glu Val Val Lys His Arg Gly Ile Pro Val Phe Thr
      65              70              75              80
Phe Met Asn Lys Leu Asp Arg Asp Gly Arg Glu Pro Leu Asp Leu Leu
      85              90              95
Gln Glu Leu Glu Glu Ile Leu Gly Ile Ala Ser Tyr Pro Met Asn Trp
      100             105             110
Pro Ile Gly Met Gly Lys Ala Phe Glu Gly Leu Tyr Asp Leu Tyr Asn
      115             120             125
Gln Arg Leu Glu Leu Tyr Lys Gly Asp Glu Arg Phe Ala Ser Pro Arg
      130             135             140
Arg Trp Arg Gln Thr Phe Trp
145             150

```

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

```

Met Ala Val Ile Ala Glu Arg Lys Ala Tyr Tyr His Asp Pro Val Glu
 1              5              10              15
Asp Ala Ile Ile Met Lys Arg Glu Ile Asp Glu Gly
      20              25

```

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

```

Met Asn Glu Thr Trp Ser Arg Thr Ala Leu Thr Leu Leu Lys His Gly
 1           5           10           15
Ser Glu Val Asn Leu Glu Arg Ala Leu Ser Val Asn Gly Arg Leu Gly
          20           25           30
Gly His Val Val Thr Gly His Ile Asp Gly Thr Gly Lys Ile Ser Ser
          35           40           45
Ile Lys Lys Asp Asp Asn Ala Val Trp Tyr Gln Ile Asn Thr Gln Lys
          50           55           60
Glu Ile Leu Asp Leu Ile Val Glu Lys Gly Ser Ile Thr Ile Asp Gly
65           70           75           80
Ile Ser Leu Thr Val Ala Lys Val Ser Lys Val Asn Phe Ser Val Ser
          85           90           95
Val Ile Pro His Thr Leu Lys Gln Thr Ile Leu Lys Ser Lys Gln Val
          100          105          110
Gly Ser Thr Val Asn Leu Glu Asn Asp Ile Leu Gly Lys Tyr Val Gln
          115          120          125
Lys Leu Met Asp Asn Ser Pro Lys Ser Glu Ile Ser Lys Glu Leu Leu
          130          135          140
Tyr Gln Asn Gly Phe
145

```

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

```

Met Asn Trp Ser Ala Leu Glu Gln Gln Ile Val Asp Glu Leu Lys Ile
 1           5           10           15
Tyr Ile Ala Pro Lys Ile Phe Gly Gly Ser Ala Lys Phe Pro Val Gly
          20           25           30

```

Gly Glu Gly Ile Ser Leu Pro Asn Asp Ala Ile Arg Leu Lys Pro Tyr
 35 40 45
 Ala Phe Ser Gln Xaa Gly Xaa Asp Tyr Leu Ile Glu Ser Glu Val Ile
 50 55 60
 Tyr Pro Cys Ser Gln Glu
 65 70

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

Met Val Leu Phe Leu Val Pro Gln Leu Arg Asn Ala Tyr Gly Thr Ala
 1 5 10 15
 Ala Ile Gly Ile Ile Cys Gly Leu Tyr Trp Ala Val Ser Ser Asn Met
 20 25 30
 Thr Val Glu Ala Thr Gln Arg Leu Thr Gly Gly Gly Gly Phe Ala Ile
 35 40 45
 Gly His Gln Gln Gln Phe Ala Ile Trp Phe Val Asp Lys Val Ala Gly
 50 55 60
 Arg Phe Gly Lys Lys Glu Ser Leu Asp Asn Leu Lys Leu Pro Lys
 65 70 75 80
 Phe Leu Ser Ile Phe His Asp Thr Val Val Ala Ser Ala Thr Phe Asp
 85 90 95
 Ala Arg Ile Leu Arg Gly His Ser Phe Asn Leu Gly Ser Arg His Tyr
 100 105 110
 Val

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

```

Met Leu Ile Asn Ser Leu Asn Gln Ser Tyr Ile Ser Ala Lys Arg Ile
 1             5             10             15
Glu Glu Val Phe Ala Glu Ser Pro Glu Asn Ile His Ser Glu Leu Glu
      20             25             30
Gln Lys Gln Val Thr Ser Gly Arg Val Leu Gln Val Gln Glu Leu Thr
      35             40             45
Phe Thr Tyr Pro Asp Ala Ala Gln Pro Ser Leu Arg Asp Ile Ser Phe
      50             55             60
Asp Met Thr Gln Gly Gln Ile Leu Gly Ile Ile Gly Gly Thr Gly Ser
65             70             75             80
Gly Lys Ser Ser Leu Val Gln Leu Leu Leu Gly Leu Tyr Pro Val Asp
      85             90             95
Lys Gly Asn Ile Asp Leu Tyr Gln Asn Gly Arg Ser Pro Leu Asn Leu
      100            105            110
Glu Gln Trp Arg Ser Trp Ile Ala Tyr Val Pro Gln Lys Val Lys Leu
      115            120            125
Phe Lys Gly Thr Ile Arg Ser Asn Leu Thr Leu Gly Leu Asn Gln Glu
      130            135            140
Val Ser Asp Gln Lys Leu Trp Gln Ala Leu Glu Ile Ala Gln Ala Lys
      145            150            155            160
Asp Phe Val Ser Glu Lys Glu Gly Leu Leu Asp Ala Leu Ile Glu Ala
      165            170            175
Gly Gly Arg Asn Phe Ser Gly Gly Gln Lys Gln Arg Leu Ser Ile Ala
      180            185            190
Arg Ala Val Leu Arg Gln Ala Pro Phe Ile Ile Leu Asp Asp Ala Thr
      195            200            205
Ser Ala Leu Asp Thr Ile Thr Glu Ser Lys Leu Leu Lys Ala Ile Arg
      210            215            220
Glu Asn Phe Pro Asn Thr Ser Leu Ile Leu Ile Ser Gln Arg Thr Ser
      225            230            235            240
Thr Leu Gln Met Ala Asp Gln Ile Leu Leu Leu Glu Lys Gly Glu Leu
      245            250            255
Leu Ala Val Gly Lys His Asp Asp Leu Met Lys Ser Ser Gln Val Tyr
      260            265            270
Arg Glu Ile Asn Ala Ser Gln His Gly Lys Glu Asp
      275            280

```

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

```

Met Lys Asp Pro Glu Ser Arg Leu Tyr Ile Leu Leu Lys Asp Gly Gln
 1             5             10             15
Val Ile Gly Thr Cys Thr Val Asp Leu Ser Thr Asn Thr Asn Tyr Phe
          20             25             30
Tyr Gly Leu Ala Ile Leu Glu Pro Glu Arg Gly Lys Gly Tyr Gly Ser
          35             40             45
Tyr Leu Ala Lys Ser Leu Val Asn Gln Leu Ile Glu Gln Asn Asp Lys
          50             55             60
Glu Phe Gln Ile Ala Val Glu Asp Ser Asn Val Gly Ala Lys Arg Leu
65             70             75             80
Tyr Glu Lys Ile Gly Phe Val Lys Gln Thr Gln Val Val Tyr Leu Asn
          85             90             95
Glu Lys Gly Ala Arg Asp Ser Glu Val
          100             105

```

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

```

Met Phe Ala Leu Ser Ser Asn Lys Glu Leu Ala Glu Arg Val Ala Gln
 1             5             10             15
Glu Ile Gly Ile Glu Leu Gly Lys Ser Ser Val Arg Gln Phe Ser Asp
          20             25             30
Gly Glu Ile Gln Val Asn Ile Glu Glu Ser Ile Arg Gly Lys His Val
          35             40             45
Phe Ile Leu Gln Ser Thr Ser Ser Pro Val Asn Asp Asn Leu Leu Glu
          50             55             60

```

```

Ile Leu Ile Met Val Asp Ala Leu Lys Arg Ala Ser Ala Glu Ser Val
65              70              75              80
Asn Val Val Met Pro Tyr Tyr Gly Tyr Ala Arg Gln Asp Arg Lys Ala
            85              90              95
Arg Ala Arg Glu Pro Ile Thr Ser Lys Leu Val Ala Asn Met Leu Glu
100          105          110
Val Ala Gly Val Asp Arg Leu Leu Thr Ile Asp Leu His Ala Ala Gln
115          120          125
Ile Gln Gly Phe Phe Asp Ile Pro Val Asp His Leu Met Gly Ala Pro
130          135          140
Leu Ile Ala Asp Tyr Phe Glu Arg Pro Gly Met Val Gly Ser Asp Tyr
145          150          155          160
Val Val Val Ser Pro Asp His Gly Gly Val Thr Arg Ala Arg Lys Leu
165          170          175
Ala Glu Phe Leu Lys Thr Ser Ile Ala Ile Ile Glu Lys Arg Arg Ser
180          185          190
Val Asp Lys Met Asn Thr Ser Glu Val Met Asn Thr Ile Gly Lys Val
195          200          205
Glu Gly Asn His Leu
210

```

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

```

Met Ile Ser Phe Leu Leu Leu Val Leu Val Trp Gly Phe Tyr Ile
1              5              10              15
Gly Tyr Arg Arg Gly Leu Leu Leu Gln Val Tyr Tyr Leu Ile Ser Ala
20              25              30
Met Ala Ser Ala Phe Met Ala Gly Gln Phe Tyr Lys Gly Leu Gly Glu
35              40              45
Gln Phe His Leu Leu Leu Pro Tyr Ala Asn Ser Gln Glu Gly Gln Gly
50              55              60
Thr Phe Phe Phe Pro Ser Asp Gln Leu Phe Gln Leu Asp Lys Val Phe
65              70              75              80

```


Tyr Ala Gly Ile Gly Tyr Leu Leu Val Phe Gly Ile Val Tyr Ser Ile
 85 90 95
 Gly Arg Leu Leu Gly Leu Leu Leu His Leu Ile Pro Ser Lys Lys Leu
 100 105 110
 Gly Gly Lys Leu Phe Gln Val Ser Ala Gly Ile Leu Ser Met Leu Val
 115 120 125
 Thr Leu Phe Val Leu Gln Met Ala Leu Thr Ile Leu Ala Thr Ile Pro
 130 135 140
 Met Ala Val Ile Gln Asn Pro Leu Glu Lys Ser Ile Val Ala Lys His
 145 150 155 160
 Ile Ile Gln Ser Ile Pro Ile Thr Thr Ser Trp Leu Lys Gln Ile Trp
 165 170 175
 Val Thr Asn Leu Ile Gly
 180

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

Met Arg Ala Phe Ser Asp Phe Gly Thr Pro Met Leu Ile Gly Glu Gly
 1 5 10 15
 Tyr Arg Thr Phe Pro Val Leu Ile Tyr Thr Gln Phe Ile Ser Glu Val
 20 25 30
 Gly Gly Asn Ser Ala Phe Ala Ile Met Ala Ile Ile Ile Ala Leu Ala
 35 40 45
 Ile Phe Leu Ile Gln Lys His Ile Ala Asn Arg Tyr Ser Phe Ser Met
 50 55 60
 Asn Leu Leu His Pro Ile Glu Pro Lys Lys Thr Thr Lys Gly Lys Met
 65 70 75 80
 Ala Ala Ile Tyr Ala Thr Val Tyr Gly Ile Ile Phe Ile Ser Val Leu
 85 90 95
 Pro Gln Ile Tyr Leu Ile Tyr Thr Ser Phe Leu Lys Thr Ser Gly Met
 100 105 110
 Val Phe Val Lys Gly Tyr Ser Pro Asn Ser Tyr Lys Val Ala Phe Asn
 115 120 125

Arg Met Gly Ser Ala Ile Phe Asn Thr Ile Arg Ile Pro Leu Ile Ala
 130 135 140
 Leu Val Leu Val Val Pro Ile Tyr Asp Ile Tyr Leu Leu Pro Ser Arg
 145 150 155 160

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

Met Val Pro Tyr Ile Val Pro Gly Thr Val Leu Gly Ile Ala Phe Ile
 1 5 10 15
 Ser Ser Phe Asn Thr Gly Leu Phe Gly Ser Gly Phe Leu Met Ile Thr
 20 25 30
 Gly Thr Ala Phe Ile Leu Ile Met Ser Leu Ser Val Arg Arg Leu Pro
 35 40 45
 Tyr Thr Ile Arg Ser Ser Val Ala Ser Leu Gln Gln Ile Ala Pro Ser
 50 55 60
 Ile Glu Glu Ala Ala Gly Lys Leu Arg Lys
 65 70

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

Met Ile Phe Ile Pro Met Ala Ala Tyr Ser Ile Ala Arg Asn Met Ser
 1 5 10 15
 Lys Arg Lys Ala Phe Thr Ile His Val Tyr Pro Leu Asn Pro Arg Asn
 20 25 30

Leu Arg Thr Phe Pro Ser His His Asp Ser Asp Tyr Gly Tyr Asp Glu
 35 40 45

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

Met Lys Phe Arg Lys Leu Ala Cys Thr Val Leu Ala Gly Ala Ala Val
 1 5 10 15
 Leu Gly Leu Ala Ala Cys Gly Asn Ser Gly Gly Ser Lys Asp Ala Ala
 20 25 30
 Lys Ser Gly Gly Asp Gly Ala Lys Thr Glu Ile Thr Trp Trp Ala Phe
 35 40 45
 Pro Val Phe Thr Gln Glu Lys Thr Gly Asp Gly Val Gly Thr Tyr Glu
 50 55 60
 Lys Ser Ile Ile Gln Ala Phe
 65 70

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

Met Asn Ser Gln Gln Lys Pro Gln Glu Ile Lys Val Glu Glu Pro Val
 1 5 10 15
 Glu Ser Lys Glu Glu Thr Val Asn Gln Pro Val Glu Gln Pro Lys Val
 20 25 30
 Glu Thr Pro Ala Val Glu Lys Gln Thr Glu Pro Thr Glu Glu Pro Lys
 35 40 45

```

Val Glu Val Thr Ser Ile Pro Gln Thr Thr Arg Tyr Glu Glu Asp Leu
  50                      55                      60
Thr Lys Glu His Gly Thr Arg Glu Val Val Lys Glu Gly Lys Asn Gly
  65                      70                      75                      80
Ser Arg Thr Val Thr Thr Pro Tyr Ile Leu Asn Ala Thr Asp Gly Thr
                      85                      90                      95
Thr Thr Glu Gly Thr Ser Thr Thr Asp Glu Ala Glu Met Glu Lys Glu
                      100                      105                      110
Val Val Arg Val Gly Thr Lys Pro Lys Glu Lys Leu Ala Pro Val Leu
                      115                      120                      125
Ser Leu Thr Ser Val Thr Asp Asn Ala Met Leu Arg Ser Ala Arg Leu
                      130                      135                      140
Thr Tyr His Leu Glu Asn Thr Asp Ser Val Asp Val Lys Lys Ile His
                      145                      150                      155                      160
Ala Glu Ile Lys Asn Gly Asp Lys Val Val Lys Thr Ile Asp Leu Ser
                      165                      170                      175
Lys Glu Arg Leu Ser Asp Ala Val Asp Gly Leu Glu Leu Tyr Lys Asp
                      180                      185                      190
Tyr Lys Ile Val Thr Ser Met Thr Tyr Asp Arg Gly Asn Gly Glu Glu
                      195                      200                      205
Thr Ser Thr Leu Glu Glu Thr Pro Leu Arg Leu Asp Leu Lys Lys Val
                      210                      215                      220
Glu Leu Lys Asn Ile Gly Ser Thr Asn Leu Val Lys Val Asn Glu Asp
                      225                      230                      235                      240
Gly Thr Glu Val Ala Ser Asp Phe Leu Thr Ser Lys Pro Val Asp Val
                      245                      250                      255
Gln Asn Tyr Tyr Leu Lys Val Thr Ser Arg Asp Asn Lys Val Val Ser
                      260                      265                      270
Pro Pro Ser
                      275

```

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

```

Met Ala Val Met Lys Ile Glu Tyr Tyr Ser Gln Val Leu Asp Met Glu
 1             5             10             15
Trp Gly Val Asn Val Leu Tyr Pro Asp Ala Asn Arg Val Glu Glu Pro
      20             25             30
Glu Cys Glu Asp Ile Pro Val Leu Tyr Leu Leu His Gly Met Ser Gly
      35             40             45
Asn His Asn Ser Trp Leu Lys Arg Thr Asn Val Glu Arg Leu Leu Arg
      50             55             60
Gly Thr Asn Leu Ile Val Val Met Pro Asn Thr Ser Asn Gly Trp Tyr
65             70             75             80
Thr Asp Thr Gln Tyr Gly Phe Asp Tyr Tyr Thr Ala Leu Ala Glu Glu
      85             90             95
Leu Pro Gln Val Pro Glu Thr Leu Leu Pro
      100             105

```

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

```

Met Arg Leu Leu Ala Met Lys Met Lys Gln Ile Ser Asp Thr Thr Leu
 1             5             10             15
Lys Ile Thr Met Ser Leu Glu Asp Leu Met Asp Arg Gly Met Glu Ile
      20             25             30
Ala Asp Phe Leu Val Pro Gln Glu Lys Thr Glu Glu Phe Phe Tyr Ala
      35             40             45
Ile Leu Gly
      50

```

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

```

Met Leu Pro Ile Ile Cys Cys Gly Glu Ser Leu Glu Thr Tyr Glu Ala
 1             5             10             15
Gly Lys Ala Ala Glu Phe Val Gly Ala Gln Val Ser Ala Ala Leu Ala
          20             25             30
Gly Leu Thr Ala Glu Gln Val Ala Ala Ser Val Ile Ala Tyr Glu Pro
      35             40             45
Ile Trp Ala Ile Gly Thr Gly Lys Ser Ala Ser Gln Asp Asp Ala Gln
      50             55             60
Lys Met Cys Lys Val Val Arg Asp Val Val Ala Ala Asp Phe Gly Gln
65             70             75             80
Glu Val Ala Asp Lys Val Arg Val Gln Tyr Gly Gly Ser Val Lys Pro
          85             90             95
Glu Asn Val Ala Ser Tyr Met Ala Cys Pro Asp Val Asp Gly Ala Leu
          100             105             110
Val Gly Gly Ala Ser Leu Glu Ala Glu Ser Phe Leu Ala Leu Leu Asp
          115             120             125
Phe Val Lys
      130

```

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

```

Met Phe Val Glu Ala Cys Lys Ala Val Val Arg Ala Asn Glu Glu Tyr
 1             5             10             15
Val Pro Pro Tyr Gly Ile Gly Gly Thr Leu Tyr Leu Arg Pro Leu Leu
          20             25             30
Ile Gly Val Gly Asp Ile Ile Gly Val Lys Pro Ala Glu Glu Tyr Ile
      35             40             45
Phe Thr Ile Phe Ala Met Pro Val Gly Asn Tyr Phe Lys Gly Gly Leu
      50             55             60

```

Val Pro Thr Asn Phe Leu Ile Gln Asp Glu Tyr Asp Arg Ala Ala Pro
 65 70 75 80
 Asn Gly Thr Gly Ala Ala Lys Val Gly Gly Asn Tyr Ala Ala Ser Leu
 85 90 95
 Leu Pro Gly Lys Met Ala Lys Ser Arg His Phe Ser Asp Val Ile Tyr
 100 105 110
 Leu Asp Pro Ser Thr His Thr Lys Ile Glu Glu Val Gly Ser Ala Asn
 115 120 125
 Phe Phe Gly Ile Thr Ala Asp Asn Glu Phe Val Thr Pro Leu Ser Pro
 130 135 140
 Ser Ile Leu Pro Ser Ile Thr Lys Tyr Ser Leu Leu Tyr Leu Ala Glu
 145 150 155 160
 His Arg Leu Gly Leu Thr Pro Ile Glu Gly Asp Val Pro Ile Asp Asn
 165 170 175
 Leu Asp Arg Phe Val Lys Ala Gly Ala Cys Gly Thr Ala Ala Val Ile
 180 185 190
 Ser Pro Ile Gly Gly Ile Gln His Gly Asp Asp Phe His Val Ile Leu
 195 200 205

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

Met Val Met Ile Ser Met Leu Phe Tyr Ser Glu Thr Glu Val Gly Pro
 1 5 10 15
 Val Thr Arg Lys Leu Tyr Asn Glu Leu Thr Gly Ile Gln Phe Gly Asp
 20 25 30
 Ile Glu Ala Pro Glu Gly Trp Ile Val Lys Val Asp
 35 40

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

```

Met Thr Ala Ser Pro Leu Lys Lys Ser Ile Lys Lys Lys Asn Arg Lys
 1           5           10           15
Leu Thr Asn Lys Xaa Glu Lys His Met Ser Lys Ile Ile Gly Ile Asp
      20           25           30
Leu Gly Thr Thr Asn Ser Ala Val Ala Val Leu Glu Gly Thr Glu Ser
      35           40           45
Lys Ile Ile Ala Asn Pro Glu Gly Asn Arg Thr Thr Pro Ser Val Val
      50           55           60
Ser Phe Lys Asn Gly Glu Ile Ile Val Gly Asp Ala Ala Lys Arg Gln
      65           70           75           80
Ala Val Thr Asn Pro Asp Thr Val Ile Ser Ile Lys Ser Lys Met Gly
      85           90           95
Thr Ser Glu Lys Val Ser Ala Asn Gly Lys Glu Tyr Thr Pro Gln Glu
      100          105          110
Ile Ser Ala Met Ile Leu Gln Tyr Leu Lys Gly Tyr Ala Glu Asp Tyr
      115          120          125
Leu Gly Glu Lys Val Thr Lys Ala Val Ile Thr Val Pro Ala Tyr Phe
      130          135          140
Asn Asp Ala Gln Arg Gln Ala Thr Lys Asp Ala Gly Lys Ile Ala Gly
      145          150          155          160
Leu Glu Val Xaa Arg Ile Val Asn Glu Pro Thr Ala Ala Ala Leu Ala
      165          170          175
Tyr Gly Leu Asp Lys Thr Asp Lys Glu Glu Lys Ile Leu Val Phe Asp
      180          185          190
Leu Gly Gly Gly Thr Phe Asp Val Ser Ile Leu Glu Leu Gly Asp Gly
      195          200          205
Val Phe Asp Val Leu Ser Thr Ala Gly Asp Asn Lys Leu Gly Gly Asp
      210          215          220
Asp Phe Asp Gln Lys Ile Ile Asp His Leu Val Ala Glu Phe Lys Lys
      225          230          235          240
Glu Asn Gly Ile Arg Leu Val Tyr
      245

```

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

```

Met Lys Leu Ile Val Asp Leu Ile Tyr Glu Gly Gly Phe Lys Lys Met
 1             5             10             15
Arg Gln Ser Ile Ser Asn Thr Ala Glu Tyr Gly Asp Tyr Val Ser Gly
      20             25             30
Pro Arg Val Ile Thr Glu Gln Val Lys Glu Asn Met Lys Ala Val Leu
      35             40             45
Ala Asp Ile Gln Asn Gly Lys Phe Ala Asn Asp Phe Val Asn Asp Tyr
      50             55             60
Lys Ala Gly Arg Pro Lys Leu Thr Ala Tyr Arg Glu Gln Ala Ala Asn
65             70             75             80
Leu Glu Ile Glu Lys Val Gly Ala Glu Leu Arg Lys Ala Met Pro Phe
      85             90             95
Val Gly Lys Asn Asp Asp Asp Ala Phe Lys Ile Tyr Asn
      100             105

```

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

```

Met Leu Leu Ser Ala Phe His Lys Tyr Glu Asn Gln Leu Asp Lys Val
 1             5             10             15
Arg Phe Ile Gly Leu His Thr Gly His Leu Gly Phe Tyr Thr Asp Tyr
      20             25             30
Arg Asp Phe Glu Leu Asp Lys Leu Val Thr Asn Leu Gln Leu Asp Thr
      35             40             45
Gly Ala Arg Val Ser Tyr Pro Val Leu Asn Val Lys Val Phe Leu Glu
      50             55             60
Asn Gly Glu Val Lys Ile Phe Arg Ala Leu Asn Glu Ala Ser Ile Arg
65             70             75             80

```

Arg Ser Asp Arg Thr Met Val Ala Asp Ile Val Ile Asn Gly Val Pro
 85 90 95
 Phe Glu Arg Phe Arg Gly Asp Gly Leu Thr Val Ser Thr Pro Thr Gly
 100 105 110
 Ser Thr Ala Tyr Asn
 115

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

Met Gly Ala Gln Leu Ala Arg Glu Phe Lys His Glu Ala Asp Ile Val
 1 5 10 15
 Val Gly Val Pro Asn Ser Ser Leu Ser Ala Ala Met Gly Phe Ala Glu
 20 25 30
 Glu Ser Gly Leu Pro Asn Glu Met Gly Leu Ile Lys Asn Gln Tyr Thr
 35 40 45
 Gln Arg Thr Phe Ile Gln Pro Thr Gln Glu Leu Arg Glu Gln Gly Val
 50 55 60
 Arg Met Lys Leu Ser Ala Val Ser Gly Val Val Lys Gly Lys Arg Val
 65 70 75 80
 Val Met Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Arg Arg Ile
 85 90 95
 Val Gln Leu Leu Lys Glu Ala Gly Ala Thr Glu Val His Val Ala Ile
 100 105 110
 Gly Ser Pro Ala Leu Ala Tyr Pro Cys Phe Tyr Gly Ile Asp Ile Gln
 115 120 125
 Thr Arg Gln Glu Leu Ile Ala Ala Asn His Thr Val Glu Glu Thr Arg
 130 135 140
 Gln Ile Ile Gly Ala Asp Ser Leu Thr Tyr Leu Ser Ile Asp Ser Leu
 145 150 155 160
 Ile Glu Ser Ile Gly Ile Glu Thr Asp Ala Pro Asn Gly Gly Leu Cys
 165 170 175
 Val Ala Tyr Phe Asp Gly Asp Tyr Pro Thr Pro Leu Tyr Asp Tyr Glu
 180 185 190

Glu Asp Tyr Arg Arg Ser Leu Glu Glu Lys Thr Ser Phe Tyr Lys
 195 200 205

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Met Lys Ile Leu Val Thr Gly Phe Asn Pro Phe Gly Gly Glu Lys Ile
 1 5 10 15
 Asn Pro Ala Leu Glu Ala Val Lys Leu Leu Pro Ser Glu Ile Asn Gly
 20 25 30
 Ala Glu Val Arg Trp Val Glu Ile Pro Thr Val Phe Tyr Lys Ser Ser
 35 40 45
 Glu Val Leu Glu Ala Glu Ile Leu Arg Tyr Gln Pro Asp Ala Val Leu
 50 55 60
 Cys Ile Gly Gln Ala Gly Gly Arg Thr Gly Leu Thr Pro Glu Arg Val
 65 70 75 80
 Ala Ile Asn Gln Asp Asp Ala Arg Ile Pro Asp Asn Glu Gly Asn Gln
 85 90 95
 Pro Ile Asp Thr Pro Ile Arg Ile Asp Gly Ala Ser Ala Tyr Phe Ser
 100 105 110
 Ser Leu Pro Ile Lys Ala Met Val Gln Ala Asn Lys Lys Glu Gly Leu
 115 120 125
 Thr Gly Ser Leu Phe Pro Ile Arg Ala Gly Thr Phe Val Cys Ser His
 130 135 140
 Leu Met Tyr Gln Ala Leu Tyr Leu Val Glu Lys Lys-Phe Pro Tyr Val
 145 150 155 160
 Lys Ala Gly Phe Met His Ile Pro Tyr Met Met Glu Gln Val Val Asn
 165 170 175
 Arg Pro Thr Thr Pro Thr Met Ser Leu Val Asp Ile Arg Arg Gly Ile
 180 185 190
 Glu Ala Ala Ile Gly Ala Met Ile Glu His Gly Asp Gln Glu Leu Thr
 195 200 205
 Leu Val Gly Gly Glu Ile His
 210 215

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

```

Met Leu Val Pro Lys Arg Val Lys His Arg Arg Glu Phe Arg Gly Lys
 1             5             10             15
Met Arg Gly Glu Ala Lys Gly Gly Lys Glu Val Ala Phe Gly Glu Tyr
             20             25             30
Gly Leu Gln Ala Thr Thr Ser His Trp Ile Thr Asn Arg Gln Ile Glu
             35             40             45
Ala Ala Arg Ile Ala Met Thr Arg Tyr Met Lys Arg Gly Gly Lys Val
             50             55             60
Trp Ile Lys Ile Phe Pro His Lys Ser Tyr Thr Ala Lys Ala Ile Gly
65             70             75             80
Val Arg Met Gly Ser Gly Lys Gly Ala Pro Glu Gly Trp Val Ala Pro
             85             90             95
Val Lys Arg Gly Lys Val Met Phe Glu Ile Ala Gly Val Ser Glu Glu
             100            105            110
Ile Ala Arg Glu Ala Leu Arg Leu Ala Ser His Lys Leu Pro Val
             115            120            125

```

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

```

Met Gly Trp Trp Arg Glu Thr Ile Asp Ile Val Lys Glu Asn Asp Pro
 1             5             10             15

```

Ala Ala Arg Thr Thr Leu Glu Val Leu Leu Thr Tyr Pro Gly Val Lys
 20 25 30
 Ala Leu Ala Ala His Arg Leu Ser His Phe Leu Trp Lys Tyr Asp Phe
 35 40 45
 Lys Leu Leu Ala Arg Met His Ser Gln Phe Trp Arg Phe Trp Thr Gln
 50 55 60
 Ile Glu Ile His Pro Gly Ala Gln Ile Asp Ser Gly Val Phe Ile Asp
 65 70 75 80
 His Gly Ser Gly Leu Val Ile Gly Glu Thr Ala Ile Val Glu Lys Gly
 85 90 95
 Val Leu Leu Tyr His Gly Val Thr Leu Gly Gly Thr Gly Lys Asp Cys
 100 105 110
 Gly Lys Arg His Pro Thr Val Arg Lys Gly Ala Leu Ile Ser Ala His
 115 120 125
 Ala Gln Val Ile Gly Pro Val Glu Ile Gly Glu Asn Ala Lys Val Gly
 130 135 140
 Ala Ala Ala Val Val Val Ala Asp Val Pro Ser Asp Val Thr Val Val
 145 150 155 160
 Gly Ile Pro Ala Lys Ile Val Arg Leu His Gly Lys Lys Asp Glu Pro
 165 170 175
 Val Ile His Glu Val Glu Glu Lys Arg Glu Tyr Tyr Val Asn Lys Leu
 180 185 190
 Glu Gln Ala Lys Asp Ala Ser His Arg Ser Ser Gly Leu
 195 200 205

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

Met Leu Phe Tyr Leu Leu Arg Asp Gly Lys Gly Leu Arg Asn Tyr Leu
 1 5 10 15
 Thr Gln Phe Ile Pro Ser Lys Leu Lys Glu Pro Val Gly Gln Val Leu
 20 25 30
 Ser Asp Val Asn Gln Gln Leu Ser Asn Tyr Val Arg Gly Gln Val Thr
 35 40 45

Val Ala Ile Ile Val Ala Val Met Phe Ile Ile Phe Phe Lys Ile Ile
 50 55 60
 Gly Leu Arg Tyr Ala Val Thr Leu Gly Val Thr Ala Gly Ile Leu Asn
 65 70 75 80
 Leu Val Pro Tyr Leu Gly Ser Phe Leu Ala Met Leu Pro Ala Leu Val
 85 90 95
 Leu Gly Leu Ile Ala Gly Pro Val Met Leu Leu Lys Val Val Ile Val
 100 105 110
 Phe Ile Val Glu Gln Thr Ile Glu Gly Arg Phe Val Ser Pro Leu Ile
 115 120 125
 Leu Gly Ser Gln Leu Asn Ile His Pro Ile Asn Val Leu Phe Val Leu
 130 135 140
 Leu Thr Ser Gly Ser Met Phe Gly Ile Trp Gly Val Leu Leu Gly Ile
 145 150 155 160
 Pro Val Tyr Ala Ser Ala Lys Val Val Ile Ser Ala Ile Phe Glu Trp
 165 170 175
 Tyr Lys Val Val Ser Gly Leu Tyr Glu Leu Glu Gly Glu Glu Val Lys
 180 185 190
 Ser Glu Gln
 195

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

Met Thr Lys Gln Val Pro Lys Phe Thr Lys Asp Thr Ala Gln Leu Tyr
 1 5 10 15
 Thr Cys Lys Trp Leu Leu Tyr Asn Lys Val Thr Lys Met Tyr Asp His
 20 25 30
 Thr Val Val Asn His Ser Val Arg Glu Tyr Ile Thr Asp Ser Ile Ser
 35 40 45
 Thr Asn Thr Ile Glu Glu Thr Gly
 50 55

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

```

Met Lys Lys Arg Ala Ile Val Ala Val Ile Val Leu Leu Leu Ile Gly
 1             5             10             15
Leu Asp Gln Leu Val Lys Ser Tyr Ile Val Gln Gln Ile Pro Leu Gly
          20             25             30
Glu Val Arg Ser Trp Ile Pro Asn Phe Val Ser Leu Thr Tyr Leu Gln
          35             40             45
Asn Arg Gly Ala Ala Phe Ser Ile Leu Gln Asp Gln Gln Leu Leu Phe
          50             55             60
Ala Val Ile Thr Leu Val Val Val Ile Gly Ala Ile Trp Tyr Leu His
65             70             75             80
Lys His Met Glu Asp Ser Phe Trp Met Val Leu Gly Leu Thr Leu Ile
          85             90             95
Ile Ala Gly Gly Leu Gly Asn Phe Ile Asp Arg Val Ser Gln Gly Phe
          100            105            110
Val Val Asp Met Phe His Leu Asp Phe Ile Asn Phe Ala Ile Phe Asn
          115            120            125
Val Ala Asp Asn Tyr Leu Thr Val Gly Val Ile Ile Leu Leu Ile Ala
          130            135            140
Met Leu Lys Glu Glu Ile Asn Gly Asn
145            150

```

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

```

Met Gly Ala Tyr Tyr Leu Val Met Gln Ser Leu Ser Tyr Leu Glu Tyr
 1             5             10             15
Glu Gln Gly Ile Gln Ser Thr Thr Val Arg His Leu Ile Leu Val Phe
          20             25             30
Tyr Leu Leu Phe Phe Met Gly Gly Ile Lys Lys Leu Asp Thr Tyr Leu
          35             40             45
Lys Glu Lys Leu Gln Glu Glu Leu Asn Gln Glu Gln Thr Leu Arg Tyr
          50             55             60
Arg Asp Met Glu Arg Tyr Ser Arg His Ile Glu Glu Leu Tyr Lys Glu
65             70             75             80
Ile Arg Ser Phe Arg His Asp Tyr Thr Asn Leu Leu Thr Thr Tyr Val
          85             90             95
Trp Ala Leu Lys Arg Arg Ile Trp Ser Arg
          100             105

```

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

```

Met His Val Arg Met Ile Pro Lys Ser Thr Pro Asp Thr Lys Phe Ala
 1             5             10             15
Asp Val Ala Thr His Gln Pro Glu Tyr Ser Arg Asp Asn Val Ala Gly
          20             25             30
Thr Ile Val Gly Phe Trp Thr Pro Glu Ile Phe His Gly Val Ser Val
          35             40             45
Ala Gly Tyr His Leu His Phe Ile Ser Asp Asp Leu Thr Phe Gly Gly
          50             55             60
His Val Met Asp Phe Val Ile Lys Glu Gly Ile Ile Glu Val Gly Ala
65             70             75             80
Val Asp Gln Leu Asp Gln Arg Phe Pro Val Gln Asp Arg Gln Tyr Leu
          85             90             95
Phe Ala Lys Phe Asn Val Asp Glu Met Lys Lys Asp Ile Glu Lys Ala
          100             105             110
Glu

```


(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

```

Met Ala Val Ala Lys Gly Lys Leu Thr Ile Ile Ala His Val Ala Cys
 1             5             10             15
Asn Asn Thr Lys Asp Ser Met Glu Leu Ala Arg His Ala Glu Ser Leu
      20             25             30
Gly Val Asp Ala Ile Ala Thr Asp Ser Thr Asn Leu Phe Pro Leu Ala
      35             40             45
Arg Ile Thr Gln Leu Pro Asn Thr Gly Thr Ile Ser Val Leu Gln Leu
      50             55             60
Gln Thr Gln Thr Thr
65

```

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

```

Met Gly Glu Thr Gln Ile Ile Asp Gly Leu Asp Pro Glu Tyr Lys Lys
 1             5             10             15
Arg Phe Met His His Tyr Asn Phe Pro Gln Tyr Ser Val Gly Glu Thr
      20             25             30
Gly Arg Tyr Gly Ala Pro Gly Arg Arg Glu Ile Gly His Gly Ala Leu
      35             40             45
Gly Glu Arg Ala Leu Ala Gln Val Leu Pro Ser Leu Glu Glu Phe Pro
      50             55             60

```

Tyr Ala Ile Arg Leu Val Ala Glu Val Leu Glu Ser Asn Gly Ser Ser
 65 70 75 80
 Ser Gln Ala Ser Ile Cys Ala Gly Thr Leu Ala Leu Met Ala Gly Gly
 85 90 95
 Val Pro Ile Lys Ala Pro Val Ala Gly Ile Ala Met Gly Leu Ile Ser
 100 105 110
 Asp Gly Asn Asn Tyr Thr Val Leu Thr Asp Ile Gln Gly Leu Glu Asp
 115 120 125
 His Phe Gly Asp Met Asp Phe Lys Val Ala Gly Thr Arg Asp Gly Ile
 130 135 140
 Thr Ala Leu Gln Met Asp Ile Lys Ile Gln Gly Ile Thr Ala Glu Ile
 145 150 155 160
 Leu Thr Glu Ala Leu Ala Gln Ala Lys Lys Ala Arg Phe Glu Ile Leu
 165 170 175
 Asp Val Ile Glu Ala Thr Ile Pro Glu Val Arg Pro Glu Leu Ala Pro
 180 185 190
 Thr Ala Pro Lys Ile Asp Thr Ile Lys Ile Asp Val Asp Lys Ile Lys
 195 200 205
 Ile Val Ile Gly Lys Gly Gly Glu Thr Ile Asp Lys Ile Ile Ala Glu
 210 215 220
 Thr Gly Val Lys Ile Asp Ile Asp Glu Glu Xaa Asn Val Phe Tyr Leu
 225 230 235 240
 Leu Leu Val Asp Gln Asn Ala Ile Asn Pro Cys Pro Lys Lys Leu Leu
 245 250 255
 Leu Val Trp Phe Arg Glu Pro Lys Trp Met Lys Phe Thr Val Leu Asn
 260 265 270
 Arg Ser Tyr Arg Glu Phe Gly Ala Phe Val Thr Leu
 275 280

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Met Ile Asn Asn Val Val Leu Val Gly Arg Met Thr Arg Asp Ala Glu
 1 5 10 15

```

Leu Arg Tyr Thr Pro Ser Asn Val Ala Val Ala Thr Phe Thr Leu Ala
      20                      25                      30
Val Asn Arg Thr Phe Lys Ser Gln Asn Gly Glu Arg Glu Ala Asp Phe
      35                      40                      45
Ile Asn Val Val Met Trp Arg Gln Gln Ala Glu Asn Leu Ala Asn Trp
      50                      55                      60
Ala Lys Lys Gly Ser Leu Ile Gly Val Thr Gly Arg Ile Gln Thr Arg
      65                      70                      75                      80
Ser Tyr Asp Asn Gln Gln Gly Gln Arg Val Tyr Val Thr Glu Val Val
      85                      90                      95
Ala Glu Asn Phe Gln Met Leu Glu Ser Arg Ser Val Arg Glu Gly His
      100                     105                     110
Thr Gly Gly Ala Tyr Ser Ala Pro Thr Ala Asn Tyr Ser Ala Pro Thr
      115                     120                     125
Asn Ser Val Pro Asp Phe Ser Arg Asn Glu Asn Pro Phe Gly Ala Thr
      130                     135                     140
Asn Pro Leu Asp Ile Ser Xaa Asp Asp Leu Pro Phe
      145                     150                     155

```

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

```

Met Asp Leu Val Arg Ile Leu Lys Glu Pro Arg Asn Ala Leu Val Lys
  1                      5                      10                      15
Gln Tyr Gln Thr Leu Leu Ser Tyr Asp Asp Val Glu Leu Glu Phe Asp
      20                      25                      30
Asp Glu Ala Leu Gln Glu Ile Ala Asn Lys Ala Ile Glu Arg Lys Thr
      35                      40                      45
Gly Ala Arg Gly Leu Arg Ser Ile Ile Glu Glu Thr Met Leu Asp Val
      50                      55                      60
Met Phe Glu Val Pro Ser Gln Glu Asn Val Lys Leu Val Arg Ile Thr
      65                      70                      75                      80
Lys Glu Thr Val Asp Gly Thr Asp Lys Pro Ile Leu Glu Thr Ala
      85                      90                      95

```

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

```

Met Thr Glu Ala Gly Tyr Val Gly Glu Asp Val Glu Asn Ile Leu Leu
 1              5              10              15
Lys Leu Leu Gln Val Ala Asp Phe Asn Ile Glu Arg Ala Glu Arg Gly
      20              25              30
Ile Ile Tyr Val Asp Glu Ile Asp Lys Ile Ala Lys Lys Ser Glu Asn
      35              40              45
Val Ser Ile Thr Arg Asp Val Ser Gly Glu Gly Val Gln Gln Ala Leu
      50              55              60
Leu Lys Ile Ile Glu Gly Thr Val Ala Ser Val Pro Pro Gln Gly Gly
65              70              75              80
Arg Lys His Pro Gln Gln Val Asp Asp Ser Ser Gly Tyr Lys Lys Tyr
      85              90              95
Pro Leu His Arg Gly Trp Cys Phe
      100

```

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

```

Met Trp Pro Arg Glu Ser Arg Ser Cys Arg Leu Thr Lys Val Lys Ile
 1              5              10              15

```

Cys Gly Leu Ser Thr Lys Glu Ala Val Glu Thr Ala Val Ser Ala Gly
 20 25 30
 Ala Asp Tyr Ile Gly Phe Val Phe Ala Pro Ser Lys Arg Gln Val Thr
 35 40 45
 Leu Glu Glu Ala Ala Glu Leu Ala Lys Leu Ile Pro Ala Asp Val Lys
 50 55 60
 Lys Val Gly Val Phe Val Ser Pro Ser Arg Val Glu Leu Leu Glu Ala
 65 70 75 80
 Ile Asp Lys Val Gly Leu Asp Leu Val Gln Val His Gly Gln Val Ala
 85 90 95
 Asp Asp Leu Phe Glu Asn Leu Pro Cys Ala Ser Ile Gln Ala Val Gln
 100 105 110
 Val Asp Gly Asn Gly His Val Pro Asn Ser Gln Ala Asp Tyr Leu Leu
 115 120 125
 Phe Asp Ala Pro Val Ala Gly Ser Gly Gln Ser Phe Asp Trp Gly Gln
 130 135 140
 Leu Asp Thr Thr Gly Leu Ala Gln Pro Phe Phe Ile Ala Gly Gly Leu
 145 150 155 160
 Asn Glu Asp Asn Val Val Lys Ala Ile Gln His Phe Thr Pro Tyr Ala
 165 170 175
 Val Asp Val Ser Ser Gly Val Glu Thr Asp Gly Gln Lys Asp His Glu
 180 185 190
 Lys Ile Arg Arg Phe Ile Glu Arg Val Lys His Gly Ile Ser Gly Thr
 195 200 205
 Lys

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

Met Asn Cys Glu Ala Val Ala Leu Gly Ser Phe Cys Glu Leu Lys Ser
 1 5 10 15
 Arg Arg Gly Lys Lys Gln Lys Gly Glu Ile Leu Met Ala Val Ile Ser
 20 25 30

```

Met Lys Gln Leu Leu Glu Ala Gly Val His Phe Gly His Gln Thr Arg
   35                               40                               45
Arg Trp Asn Pro Lys Met Ala Lys Tyr Ile Phe Thr Glu Arg Asn Gly
   50                               55                               60
Ile His Val Ile Asp Leu Gln Gln Thr Val Lys Tyr Ala Asp Gln Ala
  65                               70                               75                               80
Tyr Xaa Phe Met Arg Asp Ala Ala Ala Asn Asp Ala Val Val Leu Phe
                   85                               90                               95
Val Gly Thr Lys Lys Thr Ser Ser
                   100

```

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

```

Met Val Asp Thr Asn Thr Asp Pro Asp Asp Ile Asp Val Ile Ile Pro
  1           5           10           15
Ala Asn Asp Asp Ala Ile Arg Ala Val Lys Leu Ile Thr Ala Lys Leu
   20           25           30
Ala Asp Ala Ile Ile Glu Gly Arg Gln Gly Glu Asp Ala Val Ala Val
   35           40           45

```

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

```

Met Glu Glu Leu Gly Gln Ser Tyr Gly Tyr Leu Leu Tyr Arg Thr Glu
  1           5           10           15

```

Thr Asn Trp Asp Ala Glu Glu Glu Arg Leu Arg Ile Ile Asp Gly Arg
 20 25 30
 Asp Arg Ala Gln Leu Tyr Val Asp Gly Gln Trp Val Lys Thr Gln Tyr
 35 40 45
 Gln Thr Glu Ile Gly Glu Asp Ile Phe Tyr Gln Gly Lys Lys Lys Gly
 50 55 60
 Leu Ser Arg Leu Asp Ile Leu Ile Glu Asn Met Gly Arg Val Asn Tyr
 65 70 75 80
 Gly His Lys Phe Leu Ala Asp Thr Gln Arg Lys Gly Ile Arg Thr Gly
 85 90 95
 Val Cys Lys Asp Leu His Phe Leu Leu Asn Trp Lys His Tyr Pro Leu
 100 105 110
 Pro Leu Asp Asn Pro Glu Lys Ile Asp Phe Ser Lys Gly Trp Thr Gln
 115 120 125
 Gly Gln Pro Ala Phe Tyr Ala Tyr Asp Phe Thr Val Glu
 130 135 140

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

Met Gly Lys Glu Lys Val Trp Leu Pro Arg Lys Gln Gly Leu Pro Gly
 1 5 10 15
 Leu Ala Tyr Tyr Val Ile Glu Val Ala His Lys Glu Glu Leu Leu Thr
 20 25 30
 Ile Ala Gln Arg Ala Gln Glu Val Asp Val Pro Ile Lys Trp Met Thr
 35 40 45
 Ser Ser Gln Leu Glu Ile Thr Asp Ser Asp Gly Ile Val Thr Cys Ile
 50 55 60
 Arg Leu Ala Arg
 65

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

```

Met Asn Lys Lys Gln Trp Leu Gly Leu Gly Leu Val Ala Val Ala Ala
 1             5             10             15
Val Gly Leu Ala Ala Cys Gly Asn Arg Ser Ser Arg Asn Ala Ala Ser
          20             25             30
Ser Ser Asp Val Lys Thr Lys Ala Ala Ile Val Thr Asp Thr Gly Gly
          35             40             45
Val Asp Asp Lys Ser Phe Asn Gln Ser Ala Trp Glu Val Ala Gly Leu
          50             55             60
Gly
65
  
```

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

```

Met Ser Gln Trp Asp Arg Lys Leu Asp Ala Arg Leu Ala Gln Ala Val
 1             5             10             15
Val Ser Ile Asn Ala Phe Lys Gly Val Glu Phe Gly Leu Gly Phe Glu
          20             25             30
Ala Gly Tyr Arg Lys Gly Ser Gln Val Met Asp Glu Ile Leu Trp Ser
          35             40             45
Lys Glu Asp Gly Tyr Thr Arg Arg Thr Asn Asn Leu Gly Gly Phe Glu
          50             55             60
Gly Gly Met Thr Asn Gly Gln Pro Ile Val Val Arg Gly Val Met Lys
65             70             75             80
Pro Ile Pro Thr Leu Tyr Lys Pro Leu Met Ser Val Asp Ile Glu Thr
          85             90             95
  
```


His Glu Pro Tyr Lys Ala Thr Val Glu Arg Ser Asp Pro Thr Ala Leu
 100 105 110
 Pro Ala Ala Gly Met Val Met Glu Ala Val Val Ala Thr Val Leu Ala
 115 120 125
 Gln Glu Ile Leu Glu Lys Phe Ser Ser Asp Asn Leu Glu Glu Leu Lys
 130 135 140
 Glu Ala Val Ala Lys His Arg Asp Tyr Thr Lys Asn Tyr
 145 150 155

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

Met Glu Asp Ser Asn Ser Phe Met Leu Ser His Gln Met Glu Thr Ile
 1 5 10 15
 Leu Lys Glu Ala Gly Phe Thr Lys Ala Val Ser Tyr Phe Ile Leu Glu
 20 25 30
 Leu Lys Asp Pro Ser Gln Thr Lys Val Val Thr Glu Glu Leu Gln Lys
 35 40 45
 Asn Lys Lys Tyr Thr Val Leu Ser
 50 55

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

Met Gly Lys Lys Arg Trp Ala Arg Asn Gly Phe Glu Ser Asn Asp Ala
 1 5 10 15

Ser Tyr Ala Gln Val Val Ser Leu Tyr Asp Asp Thr Ser Ile Ser Val
 20 25 30
 Ser Asn Asn Glu Thr Asp Lys Val Leu Ala Gly Ser Leu Tyr Thr Asp
 35 40 45
 Thr Asn Glu Gln Gly Leu Thr Ile Pro Ser Ser Phe Thr Lys Lys Leu
 50 55 60
 Glu
 65

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

Met Ala Met Glu Ser Gly Ala Thr Ala Val Val Ala Glu Arg Gly Gln
 1 5 10 15
 Glu Arg Ile Thr Lys Val Arg Glu Ile Leu Gly Gly Gly Ala Asp Ala
 20 25 30
 Ala Leu Glu Cys Val Gly Thr Glu Ala Ala Ile Glu Gln Ala Leu Gly
 35 40 45
 Val Leu His Asn Gly Gly Arg Met Gly Phe Val Gly Val Pro His Tyr
 50 55 60
 Asn Asn Arg Ala Leu Gly Ser Thr Phe Met Gln Asn Ile Ser Val Ala
 65 70 75 80
 Gly Gly Ala Ala Ser Ala Thr Thr Tyr Asp Lys Gln Phe Leu Leu Lys
 85 90 95
 Ala Val Leu Asp Gly Asp Ile Asn Pro Gly Arg Val Phe Thr Ser Ser
 100 105 110
 Tyr Lys Leu Glu Asp Ile Asp Gln Ala Tyr Lys Asp Met Asp Glu Arg
 115 120 125
 Lys Thr Ile Lys Ser Met Ile Val Ile Glu
 130 135

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

```

Met Lys Gln Val Val Asp Tyr Phe Leu Ser Gln Gly Met Asp Arg Ile
 1             5             10             15
Gly Ile Leu Thr Gly Leu Glu Glu Thr Thr Asp Gln Glu Glu Ile Ile
             20             25             30
Gln Asp Lys Arg Leu Glu Asn Phe Lys Asn Tyr Ser Gln Ala Arg Gly
             35             40             45
Ile Tyr His Asp Glu Leu Val Phe Gln Gly Arg Phe Thr Ala Gln Ser
 50             55             60
Gly Tyr Asp Leu Met Lys Glu Ala Ile Gln Ser Leu Gly Asp Gln Leu
65             70             75             80
Pro Pro Ala Phe Phe Ala Ala Ser Asp Ser Leu Ala Ile Gly Ala Leu
             85             90             95
Arg Ala Leu Gln Glu Ala Gly Ile Ser Leu Pro Asp Arg Val Ser Leu
             100            105            110
Ile Phe Leu Leu Thr Thr Leu Ser Leu Thr Lys Gln Val Tyr Pro Pro
             115            120            125
Leu Ser
             130

```

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

```

Met Ala Lys Val Thr Ile Met Leu Ala Cys Ala Ala Gly Met Ser Thr
 1             5             10             15
Ser Leu Leu Val Thr Lys Met Gln Lys Ala Ala Glu Asp Lys Gly Leu
             20             25             30

```

```

Asp Ala Glu Ile Phe Ala Val Pro Ala Pro Glu Ala Glu Ile Val
   35                               40                               45
Ala Thr Lys Glu Val Asn Val Leu Leu Leu Gly Pro Gln Val Arg Tyr
   50                               55                               60
Leu Leu Gly Asp Phe Gln Glu Lys Leu Lys Asp Arg Gln Ile Pro Val
  65                               70                               75                               80
Ala Val Ile Pro Met Thr Asp Tyr Gly Met Met Asn Gly Ser Lys Val
           85                               90                               95
Leu Asp Leu Ala Glu Ser Leu Leu Asp
           100                               105

```

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

```

Met His Gly Ala Gly Val Asn Glu Pro Val Ala Glu Leu Ser Val Ala
  1                               5                               10                               15
Glu Gln Leu Leu Glu Ala Gly Ala Asp Val Ile Leu Val Pro Ala Val
           20                               25                               30
Gly Thr Val Pro Ala Phe His Asp Gln Glu Leu Arg Glu Val Val Asp
           35                               40                               45
Leu Val His Ser Lys Gly Gly Leu Val Leu Ser Ala Ile Gly Thr Ser
           50                               55                               60
Gln Glu Thr Ser Asp Thr Asp Thr Ile Lys Glu Ile Ala Leu Arg Asn
  65                               70                               75                               80
Lys Ile Cys Gly Val Asp Ile Gln His Ile Gly Asp Ala Gly Tyr Gly
           85                               90                               95
Gly Leu Ala Thr Val Asp Asn Ile Tyr Ala Leu Ser Lys Ala Ile Arg
           100                               105                               110
Gly Val Arg His Thr Val Ser Arg Leu Ala Arg Ser Val Asn Arg
           115                               120                               125

```

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

```

Met Ser Ala Ile Asn Leu Ala Ser Val Pro Lys Glu Ser Leu Thr Gln
 1             5             10             15
Val Leu Pro Arg Asp Leu His Ala Glu Tyr Phe Ala Val Leu Ala Ser
      20             25             30
Ile Ala Thr Ser Ile Glu Arg Met Ala Thr Glu Ile Arg Gly Leu Gln
      35             40             45
Lys Ser Glu Gln Arg Glu Val Glu Glu Phe Phe Ala Lys Gly Gln Lys
 50             55             60
Gly Ser Ser Ala Met Pro His Lys Arg Asn Pro Ile Gly Ser Glu Asn
65             70             75             80
Met Thr Gly Leu Ala Arg Val Ile Arg Gly His Met Ile Thr Ala Tyr
      85             90             95
Glu Asn Val Ala Leu Trp His Glu Arg Asp Ile Ser His Ser Ser Ala
      100            105            110
Glu Arg Ile Ile Thr Pro Asp Thr Thr Ile Leu Ile Asp Tyr Met Leu
      115            120            125
Asn Arg Phe Gly Asn Ile Val Lys Asn Leu Thr Val Phe Pro Glu Asn
      130            135            140
Met Ile Arg Asn Met Asn Ser Thr Phe Gly Leu Ile Phe Ser Gln Arg
      145            150            155            160
Ala Met Leu Thr Leu Ile Glu Lys Gly Met Thr Arg Glu Gln Ala Tyr
      165            170            175
Asp Leu Val Gln Pro Lys Thr Ala Tyr Ser Trp Asp Asn Gln Val Asp
      180            185            190
Phe Lys Pro Leu Leu Glu Ala Asp Ser Glu Val Thr Ser Arg Leu Thr
      195            200            205
Gln Glu Glu Ile Asp Glu Ile Phe Asn Pro Val Tyr Tyr Thr Lys Arg
      210            215            220
Val Asp Asp Ile Phe Glu Arg Leu Gly Leu Gly Asp
      225            230            235

```

(2) INFORMATION FOR SEQ ID NO:301:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

```

Met Leu Asn Leu Thr His Val Thr Leu Lys Thr Arg Gln Val Ile Leu
 1             5             10             15
Gln Asp Ala Asp Phe Thr Phe Lys Lys Gly Arg Ile Tyr Gly Leu Leu
          20             25             30
Ala Ile Asn Gly Ser Gly Lys Thr Thr Leu Phe Arg Ala Met Ser Lys
          35             40             45
Leu Leu Pro Leu Ser Ser Gly His Ile Ala Val Pro Pro Ser Leu Phe
          50             55             60
Tyr Tyr Glu Ser Val Glu Trp Leu Asp Gly Asn Leu Ser Gly Met Asp
65             70             75             80
Tyr Leu Arg Leu Ile Lys Lys His Leu Glu Val Arg Pro Lys Leu Glu
          85             90             95
Arg

```

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

```

Met Tyr Thr Leu Gly Gln Pro Asn Glu Leu Ala Ala Glu Phe Leu Asn
 1             5             10             15
Phe Val Leu Ser Asp Glu Thr Gln Glu Gly Ile Val Lys Gly Leu Lys
          20             25             30
Tyr Ile Pro Ile Lys Glu Met Lys Val Glu Lys Asp Ala Ala Gly Thr
          35             40             45
Val Thr Val Leu Glu Gly Arg Gln
          50             55

```

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

```

Met Asn Gln Glu Glu Leu Ala Lys Lys Met Leu Leu Pro Ser Lys Asn
 1             5             10             15
Ser Arg Leu Glu Lys Leu Gly Lys Gly Leu Thr Phe Ala Cys Leu Ser
          20             25             30
Leu Ile Val Ile Leu Val Ala Met Ile Leu Val Phe Val Ala Gln Lys
          35             40             45
Gly Leu Ser Thr Phe Phe Val Asn Gly Val Asn Ile Phe Asp Phe Leu
 50             55             60
Leu Gly Gly Thr Trp Asn Pro Ser Ser Lys Glu Phe Gly Ala Leu Pro
 65             70             75             80
Met Ile Leu Gly Ser Phe Ile Val Thr Ile Leu Ser Ala Leu Ile Ala
          85             90             95
Thr Pro Phe Ala Ile Gly Ala Ala Val Phe Met Thr Glu Val Ser Pro
          100             105             110
Lys Gly Ala Lys Ile Leu Gln Pro Ala Ile Glu Leu Leu Val Gly Ile
          115             120             125
Pro Ser Val Val Tyr Gly Phe Ile Gly Leu Gln Val Val Val Pro Phe
          130             135             140
Val Arg Ser Val Phe Gly Gly Thr Gly Phe Gly Ile Leu Ser Gly Ile
          145             150             155             160
Ser Val Leu Phe Val Met Ile Leu Pro Thr Val Thr Phe Met Thr Thr
          165             170             175
Asp Ser Leu Arg Ala Val Pro Xaa Leu Leu Ser
          180             185

```

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

```

Met Thr Glu Ile Arg Leu Glu His Val Ser Tyr Ala Tyr Gly Gln Glu
 1             5             10             15
Arg Ile Leu Glu Asp Ile Asn Leu Gln Val Thr Ser Gly Glu Val Val
      20             25             30
Ser Ile Leu Gly Pro Ser Gly Val Gly Lys Thr Thr Leu Phe Asn Leu
      35             40             45
Ile Ala Gly Ile Leu Glu Val Gln Ser Gly Arg Ile Val Leu Asp Gly
      50             55             60
Glu Glu Asn Pro Lys Gly His Val Ser Tyr Met Leu Gln Lys Asp Leu
      65             70             75             80
Leu Leu Glu His Lys Thr Val Leu Gly Asn Ile Ile Leu Pro Leu Leu
      85             90             95
Ile Gln Lys Val Asp Lys Ala Glu Ala Ile Ser Arg Ala Asp Lys Ile
      100             105             110
Leu Ala Thr Phe Gln Leu Thr Ala Val Arg Asp Lys Tyr Pro His Glu
      115             120             125
Leu Ser Gly Gly Met Arg Gln Arg Val Ala Leu Leu Arg Thr Tyr Leu
      130             135             140
Phe Gly His Lys Leu Phe Leu Leu Asp Glu Ala Phe Ser Ala Leu Asp
      145             150             155             160
Glu Met Thr Lys Met Glu Leu His Ala Trp Tyr Leu Glu Ile His Lys
      165             170             175
Gln Leu Gln Leu Thr Thr Leu Ile Xaa Thr His Ser Ile Glu Glu Ala
      180             185             190
Leu Xaa Leu Ser Asp Arg Ile Tyr Ile Leu Xaa Asn Xaa Pro Gly Gln
      195             200             205
Ile Val Ser Glu Ile Lys Leu Asp Trp Ser Glu Asp Glu Asp Xaa Glu
      210             215             220
Val Xaa Lys Ile Ala Xaa Lys Arg Gln Ile Leu Ala Glu Leu Gly Leu
      225             230             235             240
Asp Lys

```

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

```

Met Glu His Pro Xaa Glu Ala Ala Asp Ile Leu Ile Lys Asn Ala Pro
 1             5             10             15
Glu Leu Lys Glu Lys Arg Asp Phe Val Ile Glu Ser Gln Lys Tyr Leu
          20             25             30
Ser Lys Glu Tyr Ala Ser Asp Lys Glu Lys Trp Gly Gln Phe Asp Ala
          35             40             45
Ala Arg Trp Asn Ala Phe Tyr Lys Trp Asp Lys Glu Asn Gly Ile Leu
          50             55             60
Lys Glu Asp Leu Thr Asp Lys Gly Phe Thr Asn Glu Phe Val Lys
65             70             75

```

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

```

Met Val Tyr Thr Ser Leu Ser Ser Lys Asp Gly Asn Tyr Pro Tyr Gln
 1             5             10             15
Leu Asn Ile Ala His Leu Tyr Gly Asn Leu Met Asn Thr Tyr Gly Asp
          20             25             30
Asn Gly Asn Ile Leu Met Leu Lys Tyr Val Ala Glu Lys Leu Gly Thr
          35             40             45
His Val Thr Val Asp Ile Val Ser Leu His Asp Asp Phe Asp Glu Asn
          50             55             60
His Tyr Asp Ile Ala Phe Phe Gly Gly Gly Gln Asp Phe Glu Gln Ser
65             70             75             80
Ile Ile Ala Asp Asp Leu Pro Ala Lys Lys Glu Ser Ile Asp Asn Tyr
          85             90             95
Ile Gln Asn Asp Gly Val Val Leu Ala Ile Cys Gly Gly Phe Gln Leu
          100            105            110
Leu Gly Gln Tyr Tyr Val Glu Ala Ser Gly Lys Arg Ile Glu Gly Leu
          115            120            125

```

Gly Val Met Gly His Tyr Thr Leu Asn Gln Thr Asn Asn Arg Phe Ile
 130 135 140
 Gly Asp Ile Lys Ile His Asn Glu Arg Phe Arg
 145 150 155

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

Met His Gln His Ser Pro His Thr Ala Ser Tyr Thr Ser Ser Arg Asp
 1 5 10 15
 Ala Met Ser Lys Tyr Pro Glu Arg Cys Thr Thr Val Gly Leu Arg Leu
 20 25 30
 Asn Glu Glu Ser Asp Phe Glu Leu Tyr Ala Pro Tyr Gly Leu Glu Asp
 35 40 45
 Ile Leu Asn Phe Lys Phe Val Gln Leu Leu Ile Ser
 50 55 60

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

Met Phe Glu Ile Phe Asn Met Gly Val Gly Leu Met Leu Ala Val Ser
 1 5 10 15
 Pro Glu Asn Val Glu Arg Val Lys Glu Leu Leu Asp Glu Ala Val Tyr
 20 25 30
 Glu Ile Gly Arg Ile Val Lys Lys Glu Asn Glu Ser Val Ile Ile Lys
 35 40 45

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

```

Met Met Val Lys Lys His Tyr Phe Lys Asp Asn Glu Glu Asp Ser Lys
 1             5             10             15
Met Arg Arg Ile Leu Leu Leu Val Ala Val Leu Leu Met Ile Pro Ser
          20             25             30
Phe Ile Ser Ala Thr Thr Leu Val Arg Glu Thr Leu Lys Lys Glu Ser
          35             40             45
Leu Lys Lys Phe Ile Ser Glu Gln Phe Gln Gly His Asn Ile Leu Lys
 50             55             60
Lys Thr Tyr Ser Lys Lys Thr His Thr Leu Lys Leu Thr Ile Ser Gly
65             70             75             80
Asn Tyr Leu Thr Glu Glu Glu Leu Asp Met Ile Ser Ser Lys Arg Gly
          85             90             95
Asp Tyr Gly Leu Ser Asp Val Ser Val Gln Val Ser Gln Leu Ser Asp
          100            105            110
Ser Glu Gln Leu Ser Lys Glu Glu Leu Val Glu Tyr Phe Phe Gln Tyr
          115            120            125
Ile Lys Asp Lys Glu Ala Lys Glu Lys Glu Lys Ala Asn Lys Phe Tyr
          130            135            140
Thr Glu Ser Glu Glu Gln
145            150

```

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

```

Met Ser Ile Glu Pro Arg Arg Arg Trp Arg Asn Ser Thr Val Cys Leu
 1             5             10             15
Glu Ala Glu Leu Tyr Gln Glu Ser Leu Val Leu Ile Gly Gly Asp Pro
      20             25             30
Gly Ile Gly Lys Ser Thr Leu Leu Leu Gln Val Ser Thr Gln Leu Ser
      35             40             45
Gln Val Gly Thr Val Leu Tyr Val Ser Gly Glu Glu Ser Ala Gln Gln
      50             55             60
Ile Lys Leu Arg Ala Glu Arg Leu Gly Asp Phe Asp Ser Glu Phe Tyr
65             70             75             80
Leu Tyr Ala Glu Thr Asn Met Gln Ser Val Arg Ala Glu Val Val Ala
      85             90             95
Tyr Pro Ala Arg Leu Ser His Tyr
      100

```

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

```

Met Ala Thr Lys Gln Lys Glu Val Thr Thr Phe Asp Val Gln Val Ala
 1             5             10             15
Glu Phe Ile Arg Asn His Lys Gln Lys Gly Thr Ala Thr Asp Asp Glu
      20             25             30
Ile Asn Ala Ser Leu Val Ile Pro Phe Thr Leu Asp Ala Asp Gly Ile
      35             40             45
Glu Asp Leu Leu Gln Arg Ile Gln Asp Ala Gly Ile Ser Ile Thr Asp
      50             55             60
Asn Glu Gly Asn Pro Ser Ala Arg Val Leu Ser Asn Glu Glu Glu Pro
65             70             75             80
Glu Leu Ser Asp Glu Asp Leu Ile Gly Ser Thr Ser Ala Lys Val Asn
      85             90             95
Asp Pro Val Arg Met Tyr Leu Lys Glu Ile Gly Val Val Pro Leu Leu
      100             105             110

```

Thr Asn Glu Glu Glu Lys Glu Leu Ala Leu Ala Val Glu Ala Gly Asp
 115 120 125
 Ile Glu Ala Lys Gln Arg Leu Ala Glu Ala Asn Leu Arg Leu Val Val
 130 135 140
 Ser Ile Ala Lys Arg Tyr Val Gly Arg Gly Xaa Gln Ser Leu Thr
 145 150 155

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

Met Met Leu Lys Pro Ser Ile Asp Thr Leu Leu Asp Lys Val Pro Ser
 1 5 10 15
 Lys Tyr Ser Leu Val Ile Leu Glu Ala Lys Arg Ala His Glu Leu Glu
 20 25 30
 Ala Gly Ala Pro Ala Thr Gln Gly Phe Lys Ser Glu Lys Ser Thr Leu
 35 40 45
 Arg Ala Leu Glu Glu Ile Glu Ser Gly Asn Val Thr Ile His Pro Asp
 50 55 60
 Pro Glu Gly Lys Arg Glu Ala Val Arg Arg Arg Ile Glu Glu Glu Lys
 65 70 75 80
 Arg Arg Lys Glu Glu Glu Glu Lys Lys Ile Lys Glu Gln Ile Ala Lys
 85 90 95
 Glu Lys Glu Asp Gly Glu Lys Ile
 100

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

```

Met Ile Arg Gln Gly Gln Met Leu Glu Tyr Ala Glu Tyr Val Gly Asn
 1             5             10             15
Tyr Tyr Gly Thr Pro Leu Thr Tyr Val Asn Glu Thr Leu Asp Lys Gly
      20             25             30
Ile Asp Val Phe Leu Glu Ile Glu Val Gln Gly Ala Leu Gln Val Lys
      35             40             45
Lys Lys Val Pro Asp Ala Val Phe Ile Phe Leu Thr Pro Pro Asp Leu
      50             55             60
Asp Glu Leu Gln Glu Arg Leu Val Gly Arg Gly Thr Asp Ser Ala Glu
65             70             75             80
Val Ile Ala Gln Arg Ile Glu Lys Ala Lys Glu Glu Ile Ala Leu Met
      85             90             95
Arg Glu Tyr Asp Tyr Ala Ile Val Asn Asp Gln Val Pro Leu Ala Ala
      100            105            110
Glu Arg Val Lys Cys Val Ile Glu Ala Glu His Phe Cys Val Asp Arg
      115            120            125
Val Ile Gly His Tyr Gln Glu Met Leu Pro Lys Ser Pro Thr Thr Arg
      130            135            140

```

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

```

Met Ser Arg Leu Leu Val Ile Gly Cys Gly Gly Val Ala Gln Val Ala
 1             5             10             15
Ile Ser Lys Ile Cys Gln Asp Ser Glu Thr Phe Thr Glu Ile Met Ile
      20             25             30
Ala Ser Arg Thr Lys Ser Lys Cys Asp Asp Leu Lys Ala Lys Leu Glu
      35             40             45
Gly Lys Thr Ser Thr Lys Ile Glu Thr Ala Ala Leu Asp Ala Asp Lys
      50             55             60
Val Glu Glu Val Ile Ala Leu Ile Glu Ser Leu Gln Thr Ser Lys Leu
65             70             75             80
Phe

```

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

```

Met His Glu Ser Phe His Val Asp Asp Pro Thr Leu Tyr Ser Arg Glu
 1             5             10             15
Trp Phe Ser Trp Ala Asn Met Met Phe Cys Glu Leu Val Leu Asp Tyr
      20             25             30
Leu Asp Ile Arg
      35

```

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

```

Met Arg Phe Tyr Phe Met Glu Asn Val Val Val His Ile Ile Ser His
 1             5             10             15
Ser His Trp Asp Arg Glu Trp Tyr Leu Pro Phe Glu Ser His Arg Met
      20             25             30
Gln Leu Val Glu Leu Phe Asp Asn Leu Phe Asp Leu Phe Glu Asn Asp
      35             40             45
Pro Glu Phe Lys Ser Phe His Leu Asp Gly Gln Thr Ile Val Leu Asp
      50             55             60
Asp
65

```

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

```

Met Leu Leu Tyr Ile Leu Ser His Ile Ala Thr Gly Ile Val Ser Gly
 1             5             10             15
Thr Cys Leu Leu Lys Ala Ile Val Cys Asn Trp Trp Asn Cys Leu Thr
      20             25             30
Ile Ser Leu Ile Ser Leu Lys Met Thr Leu Ser Ser Arg Val Ser Thr
      35             40             45
Trp Met Asp Lys Leu Leu Ser Leu Thr Thr Asn Leu Gln Ile Arg Pro
      50             55             60
Glu Asn Arg Asp Lys Val Gln Arg Tyr Ile Asp Glu Gly Lys Leu Lys
65             70             75             80
Ile Gly Pro Phe Tyr Ile Leu Gln Asp Asp Tyr Leu Ile Ser Ser Glu
      85             90             95
Ala Asn Val Arg Asn Thr Leu Ile Gly Gln Gln Glu Ala Ala Lys Trp
      100            105            110
Gly Lys Ser Thr Gln Ile Gly Tyr Phe Pro Asp Thr Phe Gly Asn Met
      115            120            125
Gly Gln Ala Pro Gln Ile Leu Gln Lys Ser Gly Ile His Val Ala Ala
      130            135            140
Phe Gly Arg Gly Val Lys Pro Ile Gly Phe Asp Asn Gln Val Leu Glu
145            150            155            160
Asp Glu Gln Phe Thr Ser Gln Phe Ser Glu Met Tyr Trp Gln Gly Val
      165            170            175
Asp Gly Ser Arg Val Leu Gly Ile Leu Phe Ala Asn Trp Tyr Ser Asn
      180            185            190
Gly Asn Glu Ile Pro Val Asp Lys Asp Glu Ala Leu Thr Phe Trp Lys
      195            200            205
Gln Lys Leu Ser Asp Val Arg Cys Leu Arg Phe Asp Gln Pro Met Val
      210            215            220
Asp Asp Glu Thr Ala Val Asn Thr Ser Leu Ser Gln Lys Lys Ser Glu
225            230            235            240
Arg Ser His Ser Val Trp Gln Met Asn Ser Ser Arg Met
      245            250

```

250

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

```

Met Thr Ile Val Gly Cys Arg Ile Asp Gly Arg Leu Ile His Gly Gln
 1             5             10             15
Val Ala Asn Leu Trp Ala Gly Lys Leu Asn Val Ser Arg Ile Met Val
          20             25             30
Val Asp Asp Glu Val Val Asn Asn Asp Ile Glu Lys Ser Gly Leu Lys
          35             40             45
Leu Ala Thr Pro Pro Gly Val Lys Leu Ser Ile Leu Pro Val Glu Lys
          50             55             60
Ala Ala Ala Asn Ile Leu Ala Gly Lys Tyr Asp Ser Gln Arg Leu Phe
65             70             75             80
Ile Val Ala Arg Lys Pro Asp Arg Phe Pro Trp Phe Gly Arg Ser Arg
          85             90             95
Cys Thr Thr

```

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

```

Met Ile Gln His Pro Arg Ile Gly Ile Arg Pro Thr Ile Asp Gly Arg
 1             5             10             15
Arg Gln Gly Val Arg Glu Ser Leu Glu Val Gln Thr Met Asn Met Ala
          20             25             30

```

(2) INFORMATION FOR SEQ ID NO:320:

(A) LENGTH: 51 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

(2) INFORMATION FOR SEQ ID NO:321:

(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

```

Met Lys Leu Glu His Lys Asn Ile Phe Ile Thr Gly Ser Ser Arg Gly
 1             5             10             15
Ile Gly Leu Ala Ile Ala His Lys Phe Ala Gln Ala Gly Ala Asn Ile
      20             25             30
Val Leu Asn Ser Arg Gly Ala Ile Ser Glu Glu Leu Leu Ala Glu Phe
      35             40             45
Ser Asn Tyr Gly Ile Lys Val Val Pro Ile Ser Gly Asp Val Ser Asp
      50             55             60
Phe Ala Asp Ala Lys Arg Met Ile Asp Gln Ala Ile Ala Glu Leu Gly
      65             70             75             80
Ser Val Asp Val Leu Val Asn Asn Ala Gly Ile Thr Gln Asp Thr Leu
      85             90             95
Met Leu Lys Met Thr Glu Ala Asp Phe Glu Lys Val Leu Lys Val Asn
      100            105            110
Leu Thr Gly Ala Phe Asn Met Thr Gln Ser Val Phe Gly Asn Arg
      115            120            125

```

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

```

Met Glu Ser Met Pro Arg Ile Gly Leu Leu Val Thr Val Glu Asn Arg
 1             5             10             15
Asp Thr Glu Thr Ile Phe Asn Ala Ala Gly Leu Asp Phe Asp Val Leu
      20             25             30
Lys Ala Ser Ala Ile Ala Tyr Ile Asn Ala Asn Thr Phe Val Gln Lys
      35             40             45
Glu Asn Ala Gly Glu Met Gly Arg Ser Val Ser Tyr His Asp Met Arg
      50             55             60
Ser Val
      65

```

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

```

Met Arg Gln Gly Gln Gly Ser Val Glu Ala Ile Phe Asn Ala Ile Asp
 1             5             10             15
Lys Phe Phe Asn Gln Ser Val Arg Leu Val Ser Tyr Thr Ile Asn Ala
      20             25             30
Val Thr Asp Gly Ile Asp Ala Gln Asp Arg Val Val Gly His Cys
      35             40             45

```

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

```

Met Val Glu Asn Pro Glu Gly Phe His Phe Asp Asp Leu Gln Leu Gln
 1             5             10             15
Thr His Ala Asp Asn Asp Ile Glu Ala Leu Val Ser Leu Ala Asn Met
      20             25             30
Asp Gly Glu Lys Val Glu Phe Asn Ala Thr Gly Thr Gly Phe Arg
      35             40             45

```

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

```

Met Asn Phe Gln Leu Ala Lys Tyr Ser Leu Leu Lys Lys Phe Ser Glu
 1             5             10             15
Asn Ile Gly Phe Thr Thr Pro Glu Glu Cys Gly Ala Ile Phe Gln Tyr
      20             25             30
Leu Ile Glu Asn Val Gln Thr Asp Arg Gln Ile Ile Tyr Ser Pro Pro
      35             40             45
Cys His Asp Glu Leu Arg Met Ala Val Ala Asn Ser Leu Ala Ala Val
      50             55             60
Lys Asn Gly Ala Gly Leu Phe Glu Glu Thr Ile His Gly Ile Arg Glu
      65             70             75             80
Arg Ala Glu Asn Ala Ala Leu Glu Glu Ile Ala Val Ala Leu Asn Ile
      85             90             95
Arg Gln Asp Tyr Tyr Gln Val Glu Thr Ser Ile Val Leu Asn Glu Thr
      100            105            110
Ile Asn Thr Ser Glu Met Val Ser Arg Phe Ser Gly Ile Pro Val Pro
      115            120            125
Lys Asn Lys Ala Val Val Gly Gly Asn Thr Phe Ser His Glu Ser Gly
      130            135            140
Ile His Gln Asp Gly Val Leu Lys Asn Pro Leu Thr Tyr Glu Ile Ile
      145            150            155            160
Thr Pro Glu Leu Val Gly Val Lys Ile Pro Leu Gly Lys Leu Ser Gly
      165            170            175
Arg His Ala Phe Val Glu Lys Leu Arg Glu Leu Ala Leu Asp Phe Thr
      180            185            190
Glu Glu Asp Ile Lys Pro Phe Phe Ala Lys Phe Lys Ala Leu Ala Asp
      195            200            205
Lys Lys
      210

```

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

```

Met Ser Gln Gln Val Lys Asn Ala His Asn Leu Tyr Ile His Ala Ile
 1           5           10           15
Gln Asp Gly Arg Val Ala Glu Ala Gln Ala Gln Ser Val Gly Asp Thr
          20           25           30
Tyr Ile Gln His Ser Thr Gly Val Pro Asp Gly Lys Glu Gly Phe Ala
          35           40           45
Ala Phe Phe Ala Asp Phe Phe Glu Arg His Pro Glu Arg Gln Ile Lys
          50           55           60
Ile Val Arg Thr Ile Glu Asp Gly Asn Leu Val Phe Val His Val Pro
65           70           75           80
Ser Ile Ser Glu Trp Trp Arg Ser Ser Met Gly Asp Asp Gly Tyr Phe
          85           90           95
Pro Cys Gly

```

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

```

Met Glu Met Gln Thr Ser Ala Gln Leu Leu Thr Asn Lys Ile Phe Leu
 1           5           10           15
Lys Asn Pro Leu Lys Ala Leu Val Glu Glu Lys Tyr Gly Ile Glu Tyr
          20           25           30
Glu Glu Phe Thr Asn Pro Trp His Ala Ala Ile Ser Ser Phe Val Ala
          35           40           45
Phe Phe Leu Arg Ser Leu Pro Pro Met Leu Ser Val Thr Ile Phe Pro
          50           55           60
Ser Glu Tyr Arg Ile Pro Ala Thr Val Leu Ile Val Gly Val Ala Leu
65           70           75           80
Leu Leu Thr Gly Tyr Thr Ser Ala Arg Leu Gly Lys Asp Pro Thr Arg
          85           90           95
Thr Ala Met Ile Arg Asn Leu Ala Ile Gly Leu Leu Thr Met Gly Val
          100          105          110
Thr Phe Leu Leu Glu Gln Leu Phe Ser Ile
          115          120

```

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

```

Met Ala Phe Phe Leu Cys Pro His Phe Arg Ser Asn His Trp Lys Ile
 1             5             10             15
Leu Thr Val Ser Asp Thr Met Glu Glu Lys Arg Leu Glu Tyr Pro Met
      20             25             30
Val Thr Phe Leu Gly Asn Pro Val Ser Phe Thr Gly Lys Gln Leu Gln
      35             40             45
Val Gly Asp Lys Ala Leu Asp Phe Ser Leu Thr Thr Thr Asp Leu Ser
      50             55             60
Lys Lys Ser Leu Ala Asp Phe Asp Gly Lys Lys Lys Val Leu Ser Val
      65             70             75             80
Val Pro Ser Ile Asp Thr Gly Ile Cys Ser Thr Gln Thr Arg Arg Phe
      85             90             95
Asn Glu Glu Leu Ala Gly Leu Asp Asn Thr Val Val Leu Thr Val Ser
      100            105            110
Met Asp Leu Pro Phe Ala Gln Lys Arg Trp Cys Gly Ala Glu Gly Leu
      115            120            125
Asp Asn Ala Ile Met Leu Ser Asp Tyr Phe Asp His Ser Phe Gly Arg
      130            135            140
Asp Tyr Ala Leu Leu Ile Asn Glu Trp His Leu Leu Ala Arg Ala Val
      145            150            155            160
Phe Val Leu Asp Thr Asp Asn Thr Ile Arg Tyr Val Glu Tyr Val Asp
      165            170            175
Asn Ile Asn Ser Glu Pro Asn Phe Glu Ala Ala Ile Ala Ala Ala Lys
      180            185            190
Ala Leu

```

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

```

Met Gly Tyr Arg Pro Ser Thr Ala Asn Ala Ile Ile His Gln Val Arg
 1             5             10             15
Glu Leu Leu Val Ser Arg Gly Tyr Thr Phe Tyr Asn Arg Lys Arg Leu
          20             25             30
Met Val Val Pro Lys Ser Val Val Lys Glu Leu Leu Gly Met Glu Leu
      35             40             45
  
```

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

```

Met Gln Ala Val Glu His Phe Ile Lys Gln Phe Val Pro Glu His Tyr
 1             5             10             15
Asp Leu Phe Leu Asp Leu Ser Arg Glu Thr Lys Thr Phe Ser Gly Lys
          20             25             30
Val Thr Ile Thr Gly Gln Ala Gln Ser Asp Arg Ile Ser Leu His Gln
      35             40             45
Lys Asp Leu Glu Ile Thr Ser Val Glu Val Ala Gly Gln Ala Arg Pro
      50             55             60
Phe Thr Val Asp His Asp Asn Glu Ala Leu His Ile Glu Leu Ala Glu
      65             70             75             80
Ala Gly Gln Val Glu Leu Val Leu Ala Phe Ser Gly Lys Ile Thr Asp
          85             90             95
Asn Met Thr Gly Ile Tyr Pro Ser Tyr Tyr Thr Val Asp Gly Val Lys
      100             105             110
Lys Glu Val Leu Ser Thr Gln Phe Glu Ser His Phe Ala Arg Glu Ala
      115             120             125
  
```

Phe Pro Cys Val Asp Glu Pro Glu Ala Lys Ala Thr Phe Asp Leu Ser
 130 135 140
 Leu Arg Phe Asp Gln Ala Glu Gly Glu Leu Ala Leu Ser Asn Met Pro
 145 150 155 160
 Glu Ile Asp Val Glu Asn Arg Lys Glu Thr Gly Ile Trp Lys Phe Glu
 165 170 175
 Thr Thr Pro Arg Met Ser Ser Tyr Leu Leu Ala Phe Val Ala Gly Asp
 180 185 190
 Leu Gln Gly Val Thr Ala Lys Thr Lys Asn Gly Thr Leu Val Gly Cys
 195 200 205
 Leu Leu Asn Gln Ser Thr Ser Thr Phe Lys Ser
 210 215

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

Met Ser Gln Glu Phe Leu Ala Arg Ile Leu Glu Gln Lys Ala Arg Glu
 1 5 10 15
 Val Glu Gln Met Lys Leu Glu Gln Ile Gln Pro Leu Arg Gln Thr Tyr
 20 25 30
 Arg Leu Ala Glu Phe Leu Lys Asn His Gln Asp Arg Leu Gln Val Ile
 35 40 45
 Ala Glu Val Lys Lys Ala Ser Pro Ser Phe Gly Glu Ile Ser Ile Ser
 50 55 60
 Met Trp Ile Leu Cys Asn Arg Pro Arg Leu Met Lys Lys Thr Glu Gln
 65 70 75 80

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

```

Met Ser Ser Phe Thr Pro Glu Asp Leu Gly Met Glu Gly Tyr Ala Met
 1           5           10           15
Glu Asp Ile Arg Gly Gly Asn Ala Gln Glu Asn Ala Glu Ile Leu Leu
 20           25           30
Ser Val Leu Lys Asn Glu Ala Ser Pro Phe Leu Glu Thr Thr Val Leu
 35           40           45
Asn Ala Gly Leu Gly Phe Tyr Ala Asn Gly Lys Ile Asp Ser Ile Lys
 50           55           60
Glu Gly Val Ala Leu Ala Arg Gln Val Ile Ala Arg Gly Lys Ala Leu
 65           70           75           80
Glu Lys Leu Arg Leu Leu Gln Glu Tyr Gln Lys
           85           90

```

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

```

Met Ile Tyr Thr Val Thr Leu Asn Pro Ser Ile Asp Tyr Ile Val Arg
 1           5           10           15
Leu Asp Gln Val Lys Val Gly Ser Val Asn Arg Met Asp Ser Asp Asp
 20           25           30
Lys Phe Ala Gly Gly Lys Gly Ile Asn Val Ser Arg Val Leu Lys Arg
 35           40           45
Leu Asn Ile Ser Asn Thr Ala Thr Gly Phe Ile Gly Gly Phe Thr Gly
 50           55           60
Lys Phe Xaa Xaa Asp Thr Leu Ala Glu Glu Glu Ile Glu Xaa Arg Phe
 65           70           75           80
Val Gln Val Ala Glu Asp Thr Arg Ile Asn Val Lys Ile Xaa Ala Asp
           85           90           95
Gln Glu Thr Glu Ile Asn Gly Thr Gly Pro Thr Val Glu Pro Val Lys
          100          105          110

```

Leu Glu Glu Leu Lys Ala Ile Leu Ser Ser Leu Thr Ala Glu Asp Thr
 115 120 125
 Val Val Phe Ala Gly Ser Ser Ala Lys Asn Leu Gly Asn Val Ile Tyr
 130 135 140
 Lys Gly Phe Asn Leu Leu Asp Ala Pro Asp Trp Cys Ala Ser Gly Leu
 145 150 155 160

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

Met Met Gln Val Tyr Phe Asp Gln Gly Ile Tyr Asn Lys Lys Ala Val
 1 5 10 15
 Phe Glu Val Tyr Phe Arg Gln Gln Pro Phe Lys Asn Gly Tyr Ala Val
 20 25 30
 Phe Ala Gly Leu Glu Arg Ile Val Asn Tyr Leu Glu Asp Leu Arg Phe
 35 40 45
 Ser Asp Ser Asp Ile Ala Tyr Leu Glu Ser Leu Gly Tyr His Gly Ala
 50 55 60
 Phe Leu Asp Tyr Leu Arg Asn Phe Lys Leu Glu Leu Thr Val Arg Ser
 65 70 75 80
 Ala Gln Glu Gly Asp Leu Val Phe Ala Asn Glu Pro Ile Val Gln Val
 85 90 95
 Glu Gly Pro Leu Ala Gln Cys Gln Leu Val Glu Thr Ala Leu Leu Asn
 100 105 110
 Ile Val Asn Tyr Gln Thr Leu Val Ala Thr Lys Ala Ala Pro Tyr Pro
 115 120 125
 Phe Gly Tyr Arg Lys
 130

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

```

Met Lys Ile Ile Ile Gln Arg Val Lys Lys Ala Gln Val Ser Ile Glu
 1             5             10             15
Gly Gln Ile Gln Gly Lys Ile Asn Gln Gly Leu Leu Leu Leu Val Gly
          20             25             30
Val Gly Pro Glu Asp Gln Glu Glu Asp Leu Asp Tyr Ala Val Arg Lys
          35             40             45
Leu Val Asn Met Arg Ile Phe Ser Asp Val Glu Gly Lys Met Asn Leu
          50             55             60
Ser Val Lys Asp Ile Glu Gly Glu Ile Leu Ser Ile Leu Ser Leu Pro
65             70             75             80
Leu Cys Gly Tyr

```

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

```

Met Ile Lys Gly Thr Ile Lys Thr Val Ser Ile Met Ala Ala Thr Ser
 1             5             10             15
Gly Phe Leu Leu Tyr Asn Glu Val Phe Phe Leu Thr Asn Gly Ala Ala
          20             25             30
Gly Thr Lys Ser Ile Ser Phe Val Ile Arg Glu Leu Ala Val Ala Ser
          35             40             45
Ser Arg Thr Gln Tyr Ala Arg Ala Asn Thr Ile Gly Val Ile Gln Ile
          50             55             60
Leu Gly Gly Met Leu Ile Ile Val Cys Ile Asn Ile Leu Phe Arg Glu
65             70             75             80
Arg Lys Arg Leu Lys Gly Gly Lys
          85

```

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

```

Met Gly Phe Gly Ile Pro Ala Ala Ile Gly Ala Lys Ile Ala Asn Pro
 1             5             10             15
Asp Lys Glu Val Val Leu Phe Val Gly Asp Gly Gly Phe Gln Met Thr
      20             25             30
Asn Gln Glu Leu Ala Ile Leu Asn Ile Tyr Lys Val Pro Ile Lys Val
      35             40             45
Val Met Leu Asn Asn His Ser Leu Gly Met Val Arg Gln Trp Gln Glu
      50             55             60
Ser Phe Tyr Glu Gly Arg Thr Ser Glu Ser Val Phe Asp Thr Leu Pro
      65             70             75             80
Asp Phe Gln Leu Met Ala Gln Ala Tyr Gly Ile Lys Asn Tyr Lys Phe
      85             90             95
Asp Asn Pro Glu Thr Leu Ala Gln Asp Leu Glu Ala Thr Thr Glu Asp
      100            105            110
Val Pro Met Leu Ile Glu Val Asp Ile Ser Arg Lys Glu Gln Val Leu
      115            120            125
Pro Met Val Pro Ala Gly Lys Ser Asn His Glu Met Leu Gly Val Lys
      130            135            140
Phe His Ala
145

```

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

```

Met Trp Leu Pro Leu Asp Arg Asn Asn Lys Gly Gln Asn Ile Ala Gly
 1             5             10             15
Ala Arg Gln Ala Ala Glu Gly Ile Phe Gly Val Asp Ala Ser Gln Leu
             20             25             30
Thr Val Pro Gln Ala Ala Phe Leu Ala Gly Leu Pro Gln Ser Pro Ile
             35             40             45
Thr Tyr Ser Pro Tyr Glu Asn Thr Gly Glu Leu Lys Asn
             50             55             60

```

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

```

Met Tyr Leu Gly Asp Leu Met Glu Lys Ala Glu Cys Gly Gln Phe Ser
 1             5             10             15
Ile Leu Ser Phe Leu Leu Gln Glu Ser Gln Thr Thr Val Lys Ala Val
             20             25             30
Met Glu Glu Thr Gly Phe Ser Lys Ala Thr Leu Thr Lys Tyr Val Thr
             35             40             45
Leu Leu Asn Asp Lys Ala Leu Asp Ser Gly Leu Glu Leu Thr Ile His
             50             55             60
Ser Glu Asp Glu Asn Leu Arg Leu Ser Ile Gly Ala Ala Thr Lys Gly
             65             70             75             80
Arg Asp Ile Pro Glu Leu Val Phe Trp Ile Val Leu Leu Asn Thr Arg
             85             90             95
Phe Trp Phe Ile Phe Ser Thr Thr Asn Ser Phe
             100             105

```

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

```

Met Lys Glu Ile Ile Glu Lys Leu Ala Lys Phe Glu Asn Leu Ser Gly
 1             5             10             15
Val Glu Met Thr Asp Val Ile Glu Arg Ile Val Thr Gly Arg Val Thr
          20             25             30
Glu Ala Gln Ile Ala Ser Leu Leu Leu Ala Leu Lys Met Lys Gly Glu
          35             40             45
Thr Pro Glu Glu Arg Thr Ala Ile Ala Gln Val Met Arg Gly His Ala
          50             55             60
Gln His Ile Pro Thr Glu Ile His Asp Ala Met Asp Asn Cys Gly Thr
          65             70             75             80
Gly Gly Asp Lys Ser Phe Ser Phe Asn Ile Ser Thr Thr Ala Ala Phe
          85             90             95
Val Leu Ala Gly Gly Gly Ile His Met Ala Lys His Gly Asn Arg Ser
          100            105            110
Ile Ser Ser Lys Ser Gly Ser Ala Asp Ser Xaa Asn Leu Gly Asn Gln
          115            120            125
Ser

```

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

```

Met Asn Val Gln Met Ser Ser Lys Thr Asn Ile Leu Arg Ala His Ala
 1             5             10             15
Glu Met Gln Asn Ile Gln Arg Arg Ala Asn Glu Glu Arg Gln Asn Leu
          20             25             30
Gln Arg Tyr Arg Ser Gln Asp Leu Ala Lys Ala Ile Leu Pro Ser Leu
          35             40             45
Asp Asn Leu Glu Arg Ala Leu Ala Val Glu Gly Leu Thr Asp Asp Val
          50             55             60

```


(2) INFORMATION FOR SEQ ID NO:344:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

(2) INFORMATION FOR SEQ ID NO:345:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

Met His Phe Asp Lys Ser Lys Phe Gly Ala Val Phe Ser Ala Pro Gly
 1 5 10 15
 Leu Tyr Glu Val Glu Val Ile Asn Asn Ala Ser Phe Gly Gln Asn Ala
 20 25 30
 Gln Tyr Glu Val Ile Gln Ser Arg Lys Leu Gly Thr Phe Ala Glu Leu
 35 40 45
 Ile Glu Met Ala Lys Ile Lys
 50 55

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Met Ile Gln Ala Val Phe Glu Arg Ala Glu Asp Gly Glu Leu Arg Ser
 1 5 10 15
 Ala Glu Ile Thr Gly His Ala Glu Ser Gly Glu Tyr Gly Leu Asp Val
 20 25 30
 Val Cys Ala Ser Val Ser Thr Leu Ala Ile Asn Phe Ile Asn Ser Ile
 35 40 45
 Glu Lys Phe Ala Gly Tyr Glu Pro Ile Leu Glu Leu Asn Glu Asp Glu
 50 55 60
 Gly Gly Tyr Leu Met Val Glu Ile Pro Lys Asp Leu Pro Ser His Gln
 65 70 75 80
 Arg Glu Met Thr Gln Leu Phe Phe Glu Ser Phe Phe Leu Gly Met Ala
 85 90 95
 Asn Leu Ser Glu Asn Ser Ser Glu Phe Val Gln Thr Arg Val Ile Thr
 100 105 110
 Glu Asn

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

```

Met Thr Ala Ile Ser Met Lys Trp Leu Asn Asp Tyr Ile Trp Pro Ala
 1             5             10             15
Glu Ser Glu Phe Thr Pro Asp Met Thr Thr Asn Ala Val Lys Glu Ala
          20             25             30
Leu Thr Glu Met Leu Gln Ser Gly Thr Thr Thr Phe Asn Asp Met Tyr
          35             40             45
Asn Pro Asn Gly Val Asp Ile Gln Gln Ile Tyr Gln Val Val Lys Thr
          50             55             60
Ser Lys Met Arg Cys Tyr Phe Ser Pro Thr Leu Phe Ser Ser Glu Thr
65             70             75             80
Glu Thr Thr Ala Glu Thr Ile Ser Arg Thr Arg Ser Ile Ile Asp Glu
          85             90             95
Ile Leu Lys Tyr Lys Asn Pro Lys Phe Gln Gly Leu Trp
          100             105

```

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

```

Met Val Arg Glu Ser Ala Glu Ser Ala Gly Phe Phe Leu Glu Thr His
 1             5             10             15
Met Val Gln Gly Glu Trp Asn Thr Cys Val Phe Lys Lys Thr Lys Asp
          20             25             30
Ile Ser Gly Val Ile Gly Gly
          35

```

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

```

Met Thr Val Asp Arg Glu Gly Phe Glu Ala Ala Met Lys Glu Gln Gln
 1             5             10             15
Glu Arg Ala Arg Ala Ser Ala Val Lys Gly Gly Ser Met Gly Met Gln
             20             25             30
Asn Gly Asn Ser Ser Lys His His Cys Arg Lys Cys Leu Gln Leu Gln
             35             40             45
Cys
  
```

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

```

Met Lys Ala Gln Leu Val Pro Ser Arg Ser Lys Tyr Leu Ile Asn Asp
 1             5             10             15
Asn Thr Val Val Leu Phe Phe Gly Thr Arg Thr Asp Tyr Thr Arg Lys
             20             25             30
Tyr Asp Leu Asp Leu Val Arg Glu Val Ala Gly Asp Gln Ile Ala Arg
             35             40             45
Arg Val Val Leu Leu Ser Asp Gln Ala Phe Gly Leu Glu Asn Val Lys
             50             55             60
Glu Val Ala Leu Gly Cys Gly Gly Val Leu Asn Asp Ile Tyr Arg Val
             65             70             75             80
Phe Pro Tyr Ile Val Tyr Ala Gln Leu Phe Ala Leu Leu Thr Ser Leu
             85             90             95
Lys Val Glu Asn Lys Pro Asp Thr Pro Ser Pro Thr Gly Thr Val Asn
             100             105             110
  
```

Arg Val Val Gln Gly Val Ile Ile His Glu Tyr Gln Lys
 115 120 125

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

Met Ala Val Asn Asn Glu Ile Gly Ser Ile Gln Xaa Ile Glu Ala Ile
 1 5 10 15
 Ser Glu Phe Leu Ala Asp Lys Pro Thr Ile Ser Phe His Val Asp Ala
 20 25 30
 Val Gln Ala Leu Ala Lys Ile Pro Thr Glu Lys Tyr Leu Thr Glu Arg
 35 40 45
 Val Asp Cys Ala Thr Phe Ser Ser His Lys Phe His Gly Val Arg Gly
 50 55 60
 Val Gly Phe Val Tyr Ile Lys Ser Gly Lys Lys Ile Thr Pro Leu Leu
 65 70 75 80
 Thr Gly Gly Gly Gln Glu Arg Asp Tyr Arg Ser Thr Thr Glu Asn Val
 85 90 95
 Ala Gly Ile Ala Ala Thr Ala Lys Ala Leu Arg Leu Ser Met Glu Lys
 100 105 110
 Leu Asp Ile Phe Arg Ser Lys Thr Gly Gln Met Lys Ala Val Ile His
 115 120 125
 Gln Ala Leu Leu Asn Tyr Pro Asp Ile Phe Val Phe Ser Asp Glu Glu
 130 135 140
 Asp Phe Ala Pro His Ile Leu Thr Phe Gly Ile Lys Gly Val Arg Gly
 145 150 155 160
 Glu Val Ile Val His Ala Phe Glu Asp Tyr Asp Ile Phe Ile Ser Thr
 165 170 175
 Thr Ser Ala Cys Ser Ser Lys Ala Gly Lys Pro Ala Gly Thr Leu Ile
 180 185 190
 Ala Met Gly Val Asp Lys Asp Lys Ala Lys Ser Ala Val Arg Leu Ser
 195 200 205
 Leu Asp Leu Glu Asn Asp Met Ser Gln Val Glu Gln Phe Leu Thr Lys
 210 215 220

Leu Lys Leu Ile Tyr Asn Gln Thr Arg Lys Val Arg
 225 230 235

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

Met Leu Val Thr Gly Ala Ile Leu Gly Val Asn Val His Ile Phe Ser
 1 5 10 15
 Pro Lys Glu Leu Phe Pro Glu Lys Glu Ile Val Glu Leu Ala Glu Gly
 20 25 30
 Phe Ala Lys Glu Ser Gly Ala His Val Leu Ile Thr Glu Asp Ala Asp
 35 40 45
 Glu Ala Val Lys Asp Ala Asp Val Leu Tyr Thr Asp Val Trp Val Ser
 50 55 60
 Met Gly Glu Glu Asp Lys Phe Ala Glu Arg Val Ala Leu Leu Lys Pro
 65 70 75 80
 Tyr Gln Val Asn Met Asp Leu Val Lys Lys Ala Gly Asn Glu Asn Leu
 85 90 95
 Ile Phe Leu His Cys Leu Pro Ala Phe His Asp Thr His Thr Val Tyr
 100 105 110
 Gly Lys Asp Val Ala Glu Lys Phe Gly Val Glu Glu Met Glu Val Thr
 115 120 125
 Asp Glu Val Phe Arg Ser Lys Tyr Ala Arg His Phe Asp Gln Ala Glu
 130 135 140
 Asn Arg Met His Thr Ile Lys Ala Val Met Ala Ala Thr Leu Gly Asn
 145 150 155 160
 Leu Tyr Ile Pro Lys Val
 165

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

```

Met Arg Leu Glu Gln Asp Cys Pro Val Phe Leu Lys Ile Lys Glu Lys
 1             5             10             15
Asp Met Ala Ser Lys Met Leu His Thr Cys Leu Arg Val Glu Asn Leu
          20             25             30
Glu Lys Ser Ile Ala Phe Tyr Gln Asp Ala Phe Gly Phe Lys Glu Leu
          35             40             45
Arg Arg Arg Asp Phe Pro Asp His Ala Phe Thr Ile Val Tyr Leu Gly
          50             55             60
Leu Glu Gly Asp Asp Tyr Glu Leu Glu Leu Thr Tyr Asn Tyr Asp His
65             70             75             80
Gly Pro Tyr Val Val Gly Asp Gly Phe Ala His Ile Ala Leu Ser Thr
          85             90             95
Pro Asp Leu Glu Ala Leu His Gln Glu His Ser Thr Lys Gly Tyr Glu
          100            105            110
Val Thr Glu Pro Asn Gly Leu Pro Gly Thr Ala Pro Asn Tyr Tyr Phe
          115            120            125
Val Lys Asp Pro Asp Gly Tyr Lys Val Glu Val Ile Arg Glu Lys
          130            135            140

```

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

```

Met Asp His Thr Ile Phe Cys Val Gly Tyr Arg Val Met Gln Lys Asp
 1             5             10             15
Leu Glu Gly Thr Leu Asp Ala Glu Lys Leu Lys Ala Ala Gly Val Pro
          20             25             30
Phe Gly Pro Leu Phe Gly Lys Ile Lys Asn Gly Gln Asp Leu Val Leu
          35             40             45

```

```

Glu Asp Gly Thr Glu Ile Lys Ala Ala Asp Tyr Ile Ser Ala Pro Arg
 50                      55                      60
Pro Gly Lys Ile Ile Thr Ile Leu Gly Asp Thr Arg Lys Thr Asp Ala
65                      70                      75                      80
Ser Val Arg Leu Ala Val Asn Ala Asp Val Leu Val His Glu Ser Thr
                      85                      90                      95
Tyr Gly Lys Gly Asp Glu Lys Ile Ala Arg Asn His Gly His Ser Thr
                      100                      105                      110
Asn Met Gln Ala Ala Gln Val Ala Val Glu Ala Gly Ala Lys Arg Leu
                      115                      120                      125
Leu Leu Asn His Ile Ser Ala Arg Phe Leu Ser Lys Asp Ile Ser Lys
                      130                      135                      140
Leu Lys Lys Asp Ala Ala Thr Ile Phe Glu Asn Val His Val Val Lys
145                      150                      155                      160
Asp Leu Glu Lys Met Glu Ile Tyr Gln Ser Gln Lys Gly
                      165                      170

```

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

```

Met Ile Gln Pro Ala Ser Leu Glu Glu Leu Ala Ser Leu Val Glu Lys
 1                      5                      10                      15
Ala Gly Lys Lys Val Phe Leu Phe Val Ala Asp Trp Cys Gly Asp Cys
                      20                      25                      30
Arg Tyr Ile Tyr Pro Ala Leu Pro Glu Ile Glu Glu Thr Asn Pro Glu
                      35                      40                      45
Phe Thr Phe Ile Arg Met Asp Arg Asp Gln Tyr Met Asp Leu Ala Lys
                      50                      55                      60
Leu Trp Asp Val Tyr Gly Ile Pro Ser Leu Val Val Leu Glu Lys Asp
65                      70                      75                      80
Lys Glu Ile Gly Arg Phe Val Asn Arg Asp Arg Lys Ser Lys Glu Gln
                      85                      90                      95
Ile Asn Asp Phe Leu Ala Gly Leu Lys
                      100                      105

```


(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

```

Met Arg Leu Gly Leu Leu Gln Val Leu Arg Leu Pro Lys Ala Phe Gln
 1             5             10             15
Leu Ile Phe Ile Gln Asp Lys Gly His Gly Asp Val Ser Ser Phe Thr
          20             25             30
Ala Ser Cys Val Thr Gly Pro Trp Ala Phe Lys Leu Val Gly Lys Gln
          35             40             45
Gly Asn Ile His
          50

```

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

```

Met Lys Thr Arg Lys Ile Pro Leu Arg Lys Ser Val Val Ser Asn Glu
 1             5             10             15
Val Ile Asp Lys Arg Asp Leu Leu Arg Ile Val Lys Asn Lys Glu Gly
          20             25             30
Gln Val Phe Ile Asp Pro Thr Gly Lys Ala Asn Gly Arg Gly Ala Tyr
          35             40             45
Ile Lys Leu Asp Asn Ala Glu Ala Leu Glu Ala Lys Lys Lys Lys Val
          50             55             60
Phe Asn Arg Ser Phe Ser Met Glu Val Glu Glu Ser Phe Tyr Asp Glu
        65             70             75             80

```

Glu

NSDOCID: <WO 9737026A1 1>

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

```

Met Ser Ser Lys Ile Ser Ile Gly Gln Leu Ile Thr Phe Asn Thr Leu
 1           5           10           15
Leu Ser Tyr Phe Thr Thr Pro Met Glu Asn Ile Ile Asn Leu Gln Thr
          20           25           30
Lys Leu Gln Ser Ala Lys Val Ala Asn Asn Arg Leu Asn Glu Val Tyr
          35           40           45
Leu Val Glu Ser Glu Phe Gln Val Gln Glu Asn Pro Val His Ser His
          50           55           60
Phe Leu Met Gly Asp Ile Glu Phe Asp Asp Leu Ser Tyr Lys Tyr Gly
65           70           75           80
Phe Gly Arg Asp Thr Leu Thr Asp Ile Asn Leu Thr Ile Lys Gln Gly
          85           90           95
Asp Lys Val Ser Leu Val Gly Val Ser Gly Ser Gly Lys Thr Thr Leu
          100          105          110
Ala Lys Met Ile Val Asn Phe Phe Glu Pro Tyr Lys Gly His Ile Ser
          115          120          125
Ile Asn His Gln Asp Ile Lys Asn Ile Asp Lys Lys Ser Leu Ala Pro
          130          135          140
Ser Tyr
145

```

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

```

Met Arg Gln Ala Pro Ala Leu Ala Gln Ala Asn Ile Glu Arg Val Val
 1           5           10           15
Val His Lys Ile Ser Lys Val Trp Glu Phe His Phe Arg Ile Phe
          20           25           30

```

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

```

Met Gln Thr Gly Trp Gln Tyr Leu Gly Asn Lys Trp Tyr Tyr Leu Arg
 1             5             10             15
Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Gln Glu Gly Thr Thr Trp
          20             25             30
Tyr Tyr Leu Asp Gln Pro Asn Gly Asp Met Lys Thr Gly Trp Gln Asn
      35             40             45
Leu Gly Asn Lys Trp Tyr Tyr Leu Arg Ser Ser Gly Ala Met Ala Thr
      50             55             60
Gly Trp Tyr Gln Glu Gly Thr Thr Trp Tyr Tyr Leu Asp Gln Pro Asn
65             70             75             80
Gly Asp Met Lys Thr Gly Trp Gln Asn Leu Gly Asn Lys Trp Tyr Tyr
          85             90             95
Leu Arg Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Gln Asp Gly Ser
          100             105             110
Thr Trp Tyr Tyr Leu Asn Ala Val Met Glu Ile
      115             120

```

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

```

Met Lys Trp Gly Ser Arg Ile Leu Leu Gly Leu Thr Pro Lys Ser Leu
 1             5             10             15

```

```

Arg Tyr Arg Ile Trp Lys Lys Ala Glu Lys Glu Met Thr Lys Tyr Asp
      20                      25                      30
Leu Ala Asp Cys Asp Gly Ile Thr Glu Leu Cys Ser Gly Pro Gly Tyr
      35                      40                      45
Met Arg Asn Lys Tyr Pro Ile Thr Ser Phe Glu Asp Asn Leu Phe Leu
      50                      55                      60
Pro Phe Glu Gly Thr Glu Met Pro Ile Pro Ile Gly Tyr Asp Val Tyr
      65                      70                      75                      80
Leu Arg Thr Ala Phe Gly Asp Tyr Met Thr Pro Pro Pro Ala Asp Lys
      85                      90                      95
Gln Val Pro His Gln Asp Ala Val Ile Ala Asp Met Asp Lys Ser Tyr
      100                     105                     110
Thr Glu Tyr Lys Gly Glu Tyr Gly Gly
      115                     120

```

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

```

Met Phe Pro Asp Ser Ile Asp Thr Met His Gln Ala Asn Glu Phe Ile
  1                      5                      10                      15
Ala Leu Asp Asp Leu Phe Arg Ala Ala Ala Ile Tyr Ala Glu Ala Ile
      20                      25                      30
Tyr Glu Leu Ile Lys
      35

```

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

```

Met Asp Glu Leu Gln Lys Arg Asn Leu Leu Gly Phe Val Phe Gln Asp
 1             5             10             15
Phe Gln Leu Phe Pro His Leu Ser Val Leu Glu Asn Leu Thr Leu Ser
          20             25             30
Pro Val Lys Thr Met Gly Met Lys Gln Glu Glu Ala Glu Lys Lys Ala
          35             40             45
Ser Gly Leu Leu Glu Gln Leu Gly Leu Gly Gly His Ala Glu Ser Tyr
          50             55             60
Pro Phe Ser Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Leu Ala Arg
65             70             75             80
Ala Met Met Ile Asp Pro Glu Ile Ile Gly Tyr Asp Glu Pro Thr Ser
          85             90             95
Ala Leu Asp Pro Glu Leu Arg Leu Glu Val Glu Lys Leu Ile Leu Gln
          100            105            110
Asn Arg Glu Leu Gly Met Thr His Ile Val Val Thr His Asp Leu Gln
          115            120            125
Phe Gly
          130

```

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

```

Met Tyr Gly Ala Asn Ser Glu Arg Leu Lys Glu Ser Leu Arg Ile Ser
 1             5             10             15
Leu Ser Pro Gln Asn Thr Val Glu Asp Leu Gln Thr Leu Ala Lys Thr
          20             25             30
Leu Lys Glu Ile Ile Gly Gly
          35

```

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

```

Met Ile Ala Arg Ser Tyr Gln Glu Met Asp Asp Leu Asp Thr Ala Tyr
 1             5             10             15
Glu His Tyr Gln Glu Leu Thr Gly Asp Leu Lys Asp Asn Pro Glu Phe
             20             25             30
Leu Glu His Tyr Ile Tyr Leu Leu Arg
          35             40

```

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

```

Met Lys His Phe Asp Thr Ile Val Ile Gly Gly Gly Pro Ala Gly Met
 1             5             10             15
Met Ala Thr Ile Ser Ser Ser Phe Tyr Gly Gln Lys Thr Leu Leu Ile
             20             25             30
Glu Lys Asn Arg Lys Leu Gly Lys Lys Leu Ala Gly Thr Gly Gly Gly
          35             40             45
Arg Cys Asn Val Thr Asn Asn Gly Ser Leu Asp Asn Leu Leu Ala Gly
          50             55             60
Ile Pro Gly Asn Gly Arg Phe Leu Tyr Ser Val Phe Ser Gln Phe Asp
        65             70             75             80
Asn His Asp Ile Ile Asn Phe Phe Thr Glu Asn Gly Val Lys Leu Lys
             85             90             95
Val Glu Asp His Gly Arg Val Phe Pro Ala Ser Asp Lys Ser Arg Thr
          100             105             110
Ile Ile Glu Ala Leu Glu Lys Lys Ile Thr Glu Leu Gly Gly Gln Val
          115             120             125

```

Ala Thr Pro Asn Arg Asn Arg Phe Cys
130 135

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

Met	Thr	Leu	Ala	Lys	Asp	Ile	Ala	Ser	His	Leu	Leu	Lys	Ile	Gln	Ala
1				5				10						15	
Val	Tyr	Leu	Lys	Pro	Glu	Glu	Pro	Phe	Thr	Trp	Ala	Ser	Gly	Ile	Lys
			20					25					30		
Ser	Pro	Ile	Tyr	Thr	Asp	Asn	Arg	Val	Thr	Leu	Ala	Tyr	Pro	Glu	Thr
		35					40					45			
Arg	Thr	Leu	Ile	Glu	Asn	Gly	Phe	Val	Glu	Ala	Ile	Lys	Glu	Ala	Phe
	50					55					60				
Pro	Glu	Val	Glu	Val	Ile	Ala	Gly	Thr	Ala	Thr	Ala	Gly	Ile	Pro	His
65					70				75					80	
Gly	Ala	Ile	Ile	Ala	Asp	Lys	Met	Asp	Leu	Pro	Phe	Ala	Tyr	Ile	Pro
				85					90					95	

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

Met	Val	Lys	Val	Leu	Ala	Ala	Cys	Gly	Asn	Gly	Met	Gly	Ser	Ser	Met
1				5				10						15	
Val	Ile	Lys	Met	Lys	Val	Glu	Asn	Ala	Leu	Arg	Lys	Leu	Asn	Gln	Thr
			20					25					30		

Asp	Phe	Thr	Val	Asn	Ser	Cys	Ser	Val	Gly	Glu	Ala	Lys	Gly	Leu	Ala
	35						40					45			
Val	Gly	Tyr	Asp	Ile	Val	Ile	Ala	Ser	Leu	His	Leu	Ile	Gln	Glu	Leu
	50					55					60				
Glu	Gly	Arg	Thr	Asn	Gly	Lys	Leu	Ile	Gly	Leu	Asp	Asn	Leu	Met	Asp
65				70					75					80	
Asp	Lys	Glu	Ile	Thr	Glu	Lys	Leu	Ser	Gln	Ala	Ile	Gln			
				85					90						

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

Met	Ser	Met	Phe	Leu	Asp	Thr	Ala	Lys	Ile	Lys	Val	Lys	Ala	Gly	Asn
1				5					10					15	
Gly	Gly	Asp	Gly	Met	Val	Ala	Phe	Arg	Arg	Glu	Lys	Tyr	Val	Pro	Asn
			20					25					30		
Gly	Gly	Pro	Trp	Gly	Gly	Asp	Gly	Gly	Arg	Gly	Gly	Asn	Val	Val	Phe
		35				40						45			
Val	Val	Asp	Glu	Gly	Leu	Arg	Thr	Leu	Met	Asp	Phe	Arg	Tyr	Asn	Arg
	50					55					60				
His	Phe	Lys	Ala	Asp	Ser	Gly	Glu	Lys	Gly	Met	Thr	Lys	Gly	Met	His
65				70					75					80	
Gly	Arg	Gly	Ala	Glu	Asp	Leu	Arg	Val	Arg	Val	Pro	Gln	Gly	Thr	Thr
				85					90				95		
Val	Arg	Asp	Ala	Glu	Thr	Gly	Lys	Val	Leu	Thr	Asp	Leu	Ile	Glu	His
			100					105					110		
Gly	Gln	Glu	Phe	Ile	Val	Ala	His	Gly	Gly	Pro	Trp	Trp	Thr	Trp	Lys
		115					120					125			
Tyr	Ser	Phe	Arg	Asp	Thr	Lys	Lys	Ser	Cys	Thr	Gly	Asn	Leu		
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

```

Met Met Lys Gly Glu Met Thr Phe Lys Gln Val His Tyr Lys Tyr Gly
 1             5             10             15
Tyr Gly Arg Asp Val Leu Ser Asp Ile Asn Leu Thr Val Pro Gln Gly
      20             25             30
Ser Lys Val Ala Phe Val Gly Ile Ser Gly Ser Gly Lys Thr Thr Leu
      35             40             45
Ala Lys Met Met Val Asn Phe Tyr Asp Pro Ser Gln Gly Glu Ile Ser
      50             55             60
Leu Gly Gly Val Asn Leu Asn Gln Ile Asp Lys Lys Ala Leu Arg Gln
65             70             75             80
Tyr Ile Ile Tyr Leu Pro Pro Gln Pro Tyr Val Phe Asn Gly Thr Ile
      85             90             95
Leu Glu Asn Leu Leu Leu Gly Ala Lys Gly Gly Asp Asp Thr Gly Lys
      100            105            110
Ile Ser Leu Thr Gly Arg Ser Glu Phe Gly Ser Glu Ile Pro Lys Arg
      115            120            125
Asn Ile Ser Lys Pro Pro Cys His Leu Glu Ile Tyr Gln Thr Glu Leu
      130            135            140
Thr Ser Asp Gly Ala Gly Ile Ser Gly Gly Gln Arg Gln Arg Ile Ala
145            150            155            160
Leu Ala Arg Ala Leu Leu Thr Asp Ala Pro Val Leu Ile Leu Asp Glu
      165            170            175
Ala Thr Asn Ser Leu Asp Ile Leu Thr Lys Lys Arg Ile Val His Tyr
      180            185            190
Leu Met Ala Leu Asp Lys Thr Phe Asp Phe His Cys Ser Pro Leu Asp
      195            200            205
Tyr Cys
      210

```

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

```

Met Ala Arg Phe Ile Glu Ile Asp Ala Lys Glu His Asp Arg Val Thr
 1             5             10             15
Ser Gln Ile Ser His Phe Pro His Ile Leu Ala Ser Ser Leu Met Glu
          20             25             30
Gln Thr Ala Val Tyr Ala Gln Glu His Glu Asn Gly Lys Ala Leu Cys
          35             40             45
Gly Arg Trp Phe Ser Arg Tyr Asp Pro Asn Cys Gly Lys Arg Ala Arg
          50             55             60
Asn Val Asp Leu His Ser Leu Val Gln
65             70

```

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

```

Met Ala His Gln Gly Gln Asp Ile Tyr Asp Phe Pro Arg Ala Met Ile
 1             5             10             15
Lys Glu Asp Asn Leu Glu Phe Ser Phe Ser Gly Leu Lys Ser Ala Phe
          20             25             30
Ile Asn Leu His His Asn Ala Glu Gln Lys Gly Glu Ser Leu Ser Thr
          35             40             45
Glu Asp Leu Cys Ala Ser Phe Gln Ala Ala Val Leu Asp Ile Leu Met
          50             55             60
Ala Lys Thr Lys Lys Ala Leu Glu Lys Tyr Pro Val Lys Thr Leu Val
65             70             75             80
Val Ala Gly Gly Val Ala Ala Asn Lys Gly Leu Arg Glu Arg Leu Ala
          85             90             95
Ala Glu Val Thr Asp Val Lys Val Ile Ile Pro Pro Leu Arg Leu Cys
          100             105             110
Gly Asp Asn Ala Gly Met Ile Ala Tyr Ala Ser Val Ser Glu Trp Asn
          115             120             125

```

285

Lys Glu Asn Phe Ala Asn Leu Asp Leu Asn Ala Lys Pro Ser Leu Ala
 130 135 140
 Phe Asp Thr Met Glu
 145

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

Met Lys Arg Ser Leu Asp Ser Arg Val Asp Tyr Ser Leu Leu Leu Pro
 1 5 10 15
 Val Phe Phe Leu Leu Val Ile Gly Val Val Ala Ile Tyr Ile Ala Val
 20 25 30
 Ser His Asp Tyr Pro Asn Asn Ile Leu Pro Ile Leu Gly Gln Gln Val
 35 40 45
 Ala Trp Ile Ala Leu Gly Leu Val Ile Gly Phe Val Val Met Leu Phe
 50 55 60
 Asn Thr Glu Phe Leu Trp Lys Val Thr Pro Phe Leu Tyr Ile Phe Arg
 65 70 75 80
 Leu Gly Thr Tyr Asp Leu Ala Asp Cys Ile Leu
 85 90

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

Met Pro Asp Asp Ile Ile Asp Ser Phe Trp Tyr Ile Ile Asp His Phe
 1 5 10 15

```

Leu Lys Asn Val Phe Glu Leu Glu Glu Glu Leu Glu Phe Gln Leu Leu
      20                      25                      30
Asn Asn Gln Gly Lys Ile Thr Phe His Phe Ser Ser Gln His Leu Pro
      35                      40                      45
Thr Ala Ile Asp Phe Asp Phe Asn His Pro Phe Asp Pro Arg Tyr Pro
      50                      55                      60
Pro Arg Val Leu Val Leu Asp Met Asp Gly Arg Glu Thr Ile Leu Leu
      65                      70                      75                      80
Pro Glu Glu Asn Asp Leu Phe
                      85

```

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

```

Met Gly Lys Lys Asp Ala Ser Ala Met His Glu Met Arg Ala Ser Phe
  1                      5                      10                      15
Ile Gln Gly Ser Ile Glu Ala Gly His Thr Ala Glu Lys Ser Glu Gln
      20                      25                      30
Val Phe Asp Val Met Glu Lys Phe Ala Gly Tyr Gly Phe Asn Arg Ser
      35                      40                      45
His Ala Tyr Ala Tyr Ser Ala Leu Ala Phe Gln Leu Ala Tyr Phe Lys
      50                      55                      60
Thr His Tyr Pro Ala Ile Phe Tyr Gln Val Met Leu Asn Tyr Ser Asn
      65                      70                      75                      80
Ser Asp Tyr Leu Ile Asp Ala Leu Glu Ala Gly Phe Glu Val Ala Ser
      85                      90                      95
Leu Ser Ile Asn Thr Ile Pro Tyr His Asp Lys Ile Ala Asn Lys Ser
      100                      105                      110
Ile Tyr Ile Gly Leu Lys Ser Ile Lys Gly Leu Gln Gln Gly Leu Gly
      115                      120                      125
Ala Leu Asp Tyr
      130

```

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

```

Met Asp Lys Lys Gln Asn Leu Thr Ser Phe Gln Glu Leu Thr Thr Thr
 1             5             10             15
Glu Leu Asn Gln Ile Thr Gly Gly Glu Trp Trp Glu Glu Leu Leu His
          20             25             30
Glu Thr Ile Leu Ser Lys Phe Lys Ile Thr Lys Ala Leu Glu Leu Pro
          35             40             45
Ile Gln Leu
          50

```

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

```

Met His Glu Met Phe Thr Ala Ile Ala Glu Ser Asp Met Lys Lys Ala
 1             5             10             15
Ala Ala Ile Gln Arg Lys Phe Ile Pro Lys Val Asn Ala Leu Phe Ser
          20             25             30
Tyr Pro Ser Pro Ala Pro Val Lys Ala Ile Leu Asn Tyr Met Gly Phe
          35             40             45
Glu Ala Gly Pro Thr Arg Leu Pro Leu Val Pro Ala Pro Glu Glu Asp
          50             55             60
Val Lys Arg Ile Ile Lys Val Val Val Asp Gly Asp Tyr Glu Ala Thr
          65             70             75             80
Lys Ala Thr Val Thr Gly Val Leu Arg Pro Asp Tyr
          85             90

```

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

```

Met Leu Asn Glu Phe Pro Ile Phe Asp Tyr Glu Asp Ile Gln Leu Ile
 1             5             10             15
Pro Asn Lys Cys Val Ile Lys Ser Arg Ala Glu Ala Asp Thr Ser Val
          20             25             30
Thr Leu Gly Asn His Thr Phe Lys Leu Pro Val Val Pro Ala Asn Met
          35             40             45
Gln Thr Ile Leu Asp Glu Asn Val Ala Glu Gln Leu Ala Lys Gly Gly
          50             55             60
Tyr Leu Tyr Thr Tyr Ala Pro Phe
65             70

```

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

```

Met Asp Ile Lys Leu Lys Asp Phe Glu Gly Pro Leu Asp Leu Leu Leu
 1             5             10             15
His Leu Val Ser Lys Tyr Gln Met Asp Ile Tyr Asp Val Pro Ile Thr
          20             25             30
Glu Val Ile Glu Gln Tyr Leu Ala Tyr Val Ser Thr Leu Gln Ala Met
          35             40             45
Arg Leu Glu Val Thr Gly Glu Tyr Met Val Met Ala Ser Gln Leu Met
          50             55             60

```

```

Leu Ile Lys Ser Arg Lys Leu Leu Pro Lys Val Ala Glu Val Thr Asp
65              70              75              80
Leu Gly Asp Asp Leu Glu Gln Asp Leu Leu Ser Gln Ile Glu Glu Tyr
              85              90              95
Arg Lys Phe Lys Leu Leu Gly Glu His Leu Glu Ala Lys His Gln Glu
              100             105             110
Thr Gly Pro Val Leu Phe Gln Ser Ala Asp Arg Val Asp Leu Arg Arg
              115             120             125
Cys Gly Ala Cys Ala
              130

```

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

```

Met Gln Ser Thr Glu Lys Lys Pro Leu Thr Ala Phe Thr Xaa Ile Ser
1              5              10              15
Thr Ile Ile Leu Leu Leu Thr Val Leu Xaa Ile Phe Pro Phe Tyr
              20              25              30
Trp Ile Leu Thr Gly Ala Phe Lys Ser Gln Pro Asp Thr Ile Val Ile
              35              40              45
Pro Pro Gln Trp Phe Pro Lys Met Pro Thr Met Glu Asn Phe Gln Gln
              50              55              60
Leu Met Val Gln Asn Pro Ala Leu Gln Trp Met Trp Asn Ser Val Phe
65              70              75              80
Ile Ser Leu Val Thr Met Phe Leu Val Cys Ala Thr Ser Ser Leu Ala
              85              90              95
Gly Tyr Val Leu Ala Xaa Lys Arg Phe Tyr Gly Xaa Arg Ile Tyr Cys
              100             105             110

```

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

```

Met Leu Phe Met Arg Asp Ser Leu Asp Ser Ile Val Glu Pro Val Leu
 1             5             10             15
Asp Glu Met Gly Arg Phe Tyr Asp Trp Thr Glu Glu Glu Lys Ala Thr
          20             25             30
Tyr Arg Ala Asp Val Lys Ala Ala Leu Ala Gln Asn Asp Leu Ala Glu
          35             40             45
Leu Lys Asn
          50

```

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

```

Met Lys Ile Lys Val Val Thr Val Gly Lys Leu Lys Glu Lys Tyr Leu
 1             5             10             15
Lys Asp Gly Ile Ala Glu Tyr Ser Lys Arg Ile Ser Arg Phe Ala Lys
          20             25             30
Phe Glu Met Ile Glu Leu Ser Asp Glu Lys Thr Pro Asp Lys Ala Ser
          35             40             45
Glu Ser Glu Asn Gln Lys Ile Leu Glu Ile Glu Gly Gln Arg Ile Leu
          50             55             60
Ser Lys Ile Ala Asp Arg Asp Phe Val Ile Val Leu Ala Ile Glu Gly
          65             70             75             80
Lys Thr Phe Phe Ser Glu Glu Phe Ser Lys Gln Leu Glu Glu Thr Ser
          85             90             95
Ile Lys Gly Xaa Ser Thr Leu Thr Phe Ile Ile Gly Gly Ser Leu Gly
          100             105             110
Leu Ser Ser Ser Val Lys Asn Arg Ala Asn Leu Ser Val Ser Phe Gly
          115             120             125

```

Arg Leu Thr Leu Pro His Gln Leu Met Arg Leu Val Leu Val Glu Gln
 130 135 140
 Ile Tyr Arg Ala Phe Thr Ile Gln Gln Gly Phe Pro Tyr His Lys
 145 150 155

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

Met Gly Ile Leu Ala Trp Cys Asp Leu Val Leu Tyr Arg Leu Trp Asp
 1 5 10 15
 Ser Phe Met Asp Leu Gly Leu Phe Ile Asn Asp Ala Trp Val Arg Lys
 20 25 30
 Lys Lys Thr Leu Asn Lys Glu Arg Lys Lys Ala Gly Lys Ala Ala Leu
 35 40 45
 Pro Glu Asn Arg Trp Ile Gln Leu Leu Gly Met Val Val Thr Phe His
 50 55 60
 Val Val Met Leu Ser Phe Leu Ile Phe Ser Gly Phe Leu Asn Asn Leu
 65 70 75 80
 Trp Phe Lys Lys

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

Met Val Met Ala Glu Asp Gln Ala Val Arg Gln Asn Arg Leu Ala Ile
 1 5 10 15

Leu Ser Gln Leu Thr Lys Lys Ala Ala Lys Phe Ala Cys Phe Asn Gln
 20 25 30
 Ile Asn Thr Lys
 35

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

Met Gly Ala Gln Pro Val Gln Asp Thr Glu Thr Ser Ser Ala Leu Ile
 1 5 10 15
 Ser Ser His Tyr Leu Asp Glu Gln Asp Leu Ser Glu Lys Leu Lys Ser
 20 25 30
 Glu Leu Gln Trp Phe Glu Leu Glu Asn Lys Leu Leu Asn Leu Trp Glu
 35 40 45
 His

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

Met Asp Glu Val Thr Ile Phe Gly Ile Asn Tyr Phe Lys Glu His Tyr
 1 5 10 15
 Pro Glu Lys Leu Ala Glu Arg Phe Lys Gln Met Lys Ile Glu Glu Glu
 20 25 30
 Ala Pro Val Ile Ile Met Asp Met Thr Arg Ala Leu Gly Phe Arg Asp
 35 40 45

Asp Tyr Asp Arg Phe Tyr Ser Leu Phe Arg Glu Gly Ser Pro
 50 55 60

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

Met Lys Val Ile Asn Gln Thr Leu Leu Glu Lys Val Ile Ile Glu Arg
 1 5 10 15
 Ser Arg Ser Ser His Lys Gly Asp Tyr Gly Xaa Leu Leu Leu Leu Gly
 20 25 30
 Gly Thr Tyr Pro Tyr Gly Val Xaa Ser Ser Trp Leu Leu
 35 40 45

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

Met Asn Trp Ile Leu Leu Gln Gly Leu Ile Cys Gln Arg Asp Ala Ser
 1 5 10 15
 Tyr Asp Met Lys Gln Asp Asp Leu Asp Lys Val Ala Asp Tyr Leu Phe
 20 25 30
 Lys Thr Glu Glu Trp Thr Met Tyr Glu Leu Ile Leu Phe Gly Asn Leu
 35 40 45
 Tyr Ser Phe Tyr Asp Val Asp Tyr Val Thr Arg Ile Gly Arg Glu Val
 50 55 60
 Met Glu Arg Glu Glu Phe Tyr Gln Glu Ile Ser Arg His Lys Arg Leu
 65 70 75 80

Val	Leu	Ile	Leu	Ala	Leu	Asn	Cys	Tyr	Gln	His	Cys	Leu	Glu	His	Ser
					85					90					95
Ser	Phe	Tyr	Asn	Ala	Asn	Tyr	Phe	Glu	Ala	Tyr	Thr	Glu	Lys	Ile	Ile
			100					105					110		
Asp	Lys	Gly	Ile	Lys	Leu	Tyr	Glu	Arg	Asn	Val	Phe	His	Tyr	Leu	Lys
		115					120					125			
Gly	Phe	Ala	Leu	Tyr	Gln	Lys	Gly	Gln	Cys	Lys	Glu	Gly	Cys	Lys	Gln
		130				135						140			
Met	Gln	Glu	Thr	Met	His	Ile	Phe	Asp	Val	Leu	Gly	Leu	Pro	Glu	Gln
145					150					155					160
Val	Ser	Leu	Leu	Ser	Gly	Thr	Leu	Arg	Lys	Ile	Cys	Gln	Lys	Leu	Ile
				165					170						175
Phe	Pro	Asn	Lys	Gly	Lys	Asn	Lys	Lys	Leu	Leu	Ser	Val	Leu	Ile	Gln
			180					185							190

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

Met	Ser	Thr	Val	Leu	Ser	Trp	Thr	Ala	Tyr	Lys	Thr	Gln	Arg	Leu	Glu
1				5					10					15	
Met	Ser	Ile	Leu	Leu	His	Met	Ile	Val	Asn	Gly	Ile	Ala	Phe	Cys	Leu
			20					25					30		
Leu	Ala	Leu	Val	Val	Ile	Met	Ser	Arg	Thr	Leu	Gly	Ile	Ser	Val	
		35					40						45		

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

```

Met Arg Glu Asn Asp Leu Leu Leu Ile Thr Ala Asp His Gly Asn Asp
 1             5             10             15
Pro Thr Tyr Ala Gly Thr Asp His Thr Arg Glu Tyr Ile Pro Leu Leu
          20             25             30
Ala Tyr Ser Pro Ala Phe Lys Gly Asn Gly Leu Ile Pro Val Gly His
          35             40             45
Phe Ala Asp Ile Ser Ala Thr Val Ala Asp Asn Phe Gly Val Glu Thr
          50             55             60
Ala Met Ile Gly Glu Ser Phe Leu Asp Lys Leu Val
65             70             75

```

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

```

Met Lys Lys Ile Phe Leu Thr Leu Leu Thr Val Ser Leu Leu Gly Gly
 1             5             10             15
Ala Ser Thr Ala Val Ala Gln Asp Phe Thr Ile Ala Ala Lys His Ala
          20             25             30
Ile Ala Val Glu Ala Asn Thr Gly Lys Ile Leu Tyr Glu Lys Asp Ala
          35             40             45
Thr Pro Pro Val Glu Ile Ala Ser Ile Thr Lys Leu Ile Thr Val Tyr
          50             55             60
Leu Val Tyr Glu Ala Leu Glu Asn Gly Ser Ile Thr Leu Ser Thr Pro
65             70             75             80
Val Asp Ile Ser Asp Tyr Pro Tyr Gln Leu Thr Thr Asn Ser Glu Ala
          85             90             95
Ser Asn Ile Pro Met Glu Ala Arg Asn Tyr Thr Val Glu Glu Leu Leu
          100            105            110
Glu Ala Thr Leu Val Ser Ser Ala Asn Ser Ala Ala Ile Ala Leu Ala
          115            120            125
Glu Lys Ile Ala Gly Ser Glu Lys Asp Phe Val Xaa Met Met Arg Ala
          130            135            140

```

Lys Leu Leu Glu Trp Gly Ile Arg Ile His Cys Cys Gln Tyr Asp Arg
 145 150 155 160
 Ser

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

Met Ser Asn Ala Met Glu Gly Val Leu Tyr Phe Leu Lys Pro Asp Phe
 1 5 10 15
 Ser Lys Leu Thr Ser Ala Asp Leu Leu Tyr Ala Leu Gly Gln Ser Phe
 20 25 30
 Phe Ala Leu Ser Leu Gly Val Thr Asp Met Leu Thr Tyr Ala Ser Tyr
 35 40 45
 Leu Asp Lys Lys Thr Asn Leu Val Gln Ser Gly Ile Ser Ile Val Thr
 50 55 60
 Met Asn Ile Ser Ile Val His His Gly Arg Ser Ser His Phe Pro Ser
 65 70 75 80
 His Val Ser Leu Gln Tyr Pro Leu
 85

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

Met Lys Val Ala Lys Pro Phe Trp Ala Ile Val Lys Leu Lys Ser Val
 1 5 10 15

Gln His Ala Ser Met Leu Glu Asn Pro Lys Glu Met Asp Gly Leu Met
 20 25 30
 Lys Gln Val Glu Asn Leu Ala Leu Glu Asn Gln Gly Tyr Gln Val Glu
 35 40 45
 Lys Glu Asn Lys Ala Phe Glu Gln Ile Lys Asp Ser Val Ala Thr Phe
 50 55 60
 Gln Thr Phe Leu Thr Ile Phe Leu Tyr Gly Cys
 65 70 75

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

Met Asp Ala Glu Val Ser Lys Asn Leu Arg Leu Ile Leu Glu Arg Lys
 1 5 10 15
 Gly Met Thr Ile Leu Thr Gly Thr Lys Leu Gln Glu Ile Ile Glu Glu
 20 25 30
 Asn Gly Gln Leu Arg Ile Lys Val Glu Gly Lys Asp Asn Ile Ile Ala
 35 40 45
 Ser Lys Ala Leu Leu Ser Ile Gly Arg Met Pro Asp Leu Glu Gly Ile
 50 55 60
 Gly Glu Val Glu Phe Glu Leu Asp Arg Gly Cys Ile Lys Val Asn Glu
 65 70 75 80
 Tyr Met Glu Thr Ser Val Pro Arg Ile Tyr Ala Thr Arg
 85 90

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

```

Met Lys Asn Ser Ile Met Asp Thr Lys Phe Asp Arg Arg Ile Leu Leu
 1             5             10             15
Leu Asn Lys Ile Ile Ile Val Phe Ile Val Leu Met Thr Leu Leu Pro
          20             25             30
Leu Leu Tyr Ile Val Val Ala Ser Phe Met Asp Pro Lys Val Leu Val
          35             40             45
Ser Arg Gly Ile Ser Phe Asn Pro Ala Asp Trp Thr Val Glu Gly Tyr
          50             55             60
Gln Arg Val Ile Gln
          65

```

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

```

Met Val Ile Pro Glu Ala Gly Tyr Leu Tyr Ala Phe His Tyr Pro Asn
 1             5             10             15
Leu Lys Gly Lys Gly Lys Glu Ala Val Gln Val Ile Tyr Asn Leu Asn
          20             25             30
Leu Ala Ser Ala Lys Val Ile Gln Leu Tyr Arg Ser Leu Gly Leu Asp
          35             40             45
Gly Lys Ile Gly Ile Ile Leu Asn Leu Thr Pro Ala Tyr Pro Arg Ser
          50             55             60
Asn Ser Pro Glu Asp Leu Glu Ala Ser Arg Phe Thr Asp Asp Phe Phe
          65             70             75             80
Asn Lys Val Phe Leu Glu Ser Ser Cys
          85

```

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

```

Met Thr Arg Ile Ala Ser Val Ser Val Ile Arg Asn Ala Ala Phe Ile
 1             5             10             15
Ala Ile Ala Leu Ser Phe Leu Gly Lys Phe Thr Ala Leu Ile Ser Thr
      20             25             30
Ile Pro Asn Ala Val Leu Gly Gly Met Ser Ile Leu Leu Tyr Gly Val
      35             40             45
Ile Ala Ser Asn Gly Leu Lys Val Leu Ile Lys Glu Arg Val Asp Phe
      50             55             60
Ala Gln Met Arg Asn Leu Ile Ile Ala Ser Ala Met Leu Val Leu Gly
65             70             75             80
Leu Gly Arg Ser Tyr Pro
      85

```

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

```

Met Ser Leu Arg Glu Lys Ser Met Ser Glu Tyr Lys Leu Ser Glu Asn
 1             5             10             15
Asn Trp Thr Arg Val Ala Val Phe Ala Gly Gly Asn Arg Gly His Tyr
      20             25             30
Arg Thr Asp Phe Asp Ala Phe Val Gly Val Asp Arg Gly Ser Leu Trp
      35             40             45
Val Leu Glu Glu Asp Leu Pro Leu Ala Leu Ala Val Gly Asp Phe Asp
      50             55             60
Ser Val Thr Glu Glu Glu Arg Gln Val Ile Gln Lys Arg Ala Gln Tyr
65             70             75             80
Phe Val Gln Ala Arg Pro Glu Lys Asp Asp Thr Asp Leu Glu Leu Ala
      85             90             95

```

Leu Leu Thr Ile Phe Glu Gln Asn Pro Gln Ala Glu Val Thr Ile Phe
 100 105 110
 Gly Ala Leu Gly Gly Arg Ile Asp His Met Leu Ala Asn Val Leu Ser
 115 120 125
 Thr

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

Met Val Leu Gln Arg Asn Glu Ile Asn Glu Lys Asp Thr Trp Asp Leu
 1 5 10 15
 Ser Thr Ile Tyr Pro Thr Asp Gln Ala Trp Glu Glu Ala Leu Lys Asp
 20 25 30
 Leu Thr Glu Gln Leu Glu Thr Val Ala Gln Tyr Glu Gly His Leu Leu
 35 40 45
 Asp Ser Ala Asp Asn Leu Leu Val Asn His
 50 55

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

Met Ile Tyr Gly Ala Ile Ile Asp Ala Lys Thr Ala Glu Asn Ala Ala
 1 5 10 15
 Gly Met Thr Ala Met Gln Thr Ala Thr Asp Asn Ala Lys Lys Val Ile
 20 25 30

301

(2) INFORMATION FOR SEQ ID NO: 402:

(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

(2) INFORMATION FOR SEQ ID NO:403:

(A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

302

Thr Glu Ser Asp Phe Glu
65 70

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

```

Met Phe Ala Ala Val Thr Ala Gly Tyr Gln Ala Ala Leu Met Val Pro
 1           5           10           15
Thr Glu Ile Leu Ala Glu Gln His Phe Glu Ser Leu Gln Asn Leu Phe
          20           25           30
Pro Asn Leu Lys Leu Ala Leu Leu Thr Gly Ser Leu Lys Ala Ala Glu
          35           40           45
Lys Arg Glu Val Leu Glu Thr Ile Ala Lys Gly Glu Ala Asp Leu Ile
          50           55           60
Ile Gly Thr His Ala Leu Ile Gln Asp Gly Val Glu Tyr Ala Arg Leu
65           70           75           80
Gly Leu Ile Ile Ile Asp Glu Gln His Arg Phe Gly Val Gly Gln Arg
          85           90           95
Arg Ile Leu Arg Glu Lys Gly Asp Asn Pro Asp Val Leu Met Met Thr
          100          105          110
Ala Thr Pro Ile Pro Arg Thr Leu Ala Ile Thr Ala Phe Gly Asp Met
          115          120          125
Asp Val Ser Ile Ile Asp Gln Met Pro Ala Gly Arg Lys Pro Tyr Cys
          130          135          140
Asp Ala Leu Asp Gln Thr
145          150

```

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

```

Met Asn Arg Glu Ala Leu Arg Leu Tyr Leu Val Thr Asn Arg Tyr Gln
 1             5             10             15
Asp Ser Val Glu Ser Phe Leu Ala Lys Val Glu Thr Ala Cys Arg Ser
      20             25             30
Gly Val Thr Ile Val Gln Leu Arg Glu Lys Asn Leu Thr Thr Asn Gln
      35             40             45
Tyr Tyr Gln Leu Ala Lys Gln Val Lys Glu Ile Thr Asp Ala Tyr Gln
      50             55             60
Val Pro Leu Ile Ile Asp Asp Arg Leu Asp Val Cys Leu Ala Val Asp
65             70             75             80
Ala Ala Gly Leu His Ile Gly Asp Asp Glu Leu Pro Val Ser Val Ala
      85             90             95
Arg Gln Val Leu Gly Pro Glu Lys Ile Pro Arg Cys His Arg
      100             105             110

```

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

```

Met Gln Gly Ser His Phe His Leu Pro Ile Tyr Arg Met Thr Ser Gln
 1             5             10             15
Ala Leu Leu Asp Glu Thr Lys Lys Val Ala Ile Pro Val Leu Ala Thr
      20             25             30
Thr Gln Ser Lys Asp Ser Val Asp Tyr Arg Glu Leu Pro Ser Ile Glu
      35             40             45
Asn Phe Val Leu Val Met Gly Asn Glu Gly Gln Gly Ile Ser Pro Leu
      50             55             60
Met Ala Glu Ser Ala Asp Gln Leu Val His Ile Ser Met Lys Gly Gln
65             70             75             80
Ala Glu Ser Leu Asn Val Ala Val Ala Ala Gly Ile Leu Ile Phe His
      85             90             95
Leu Ser

```

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

```

Met Thr Lys Thr Ala Phe Leu Phe Ala Gly Gln Gly Ala Gln Tyr Leu
 1             5             10             15
Arg Met Gly Arg Asp Phe Tyr Asp Gln Tyr Pro Ile Val Lys Glu Thr
      20             25             30
Ile Asp Arg Ala Ser Gln Val Leu Gly Tyr Asp Leu Arg Tyr Leu Ile
      35             40             45
Asp Thr Glu Glu Asp Lys Leu Asn Gln Thr Arg Tyr Thr Gln Pro Ala
      50             55             60
Ile Leu Ala Thr Ser Val Ala Ile Tyr Arg Leu Leu Gln Glu Lys Gly
      65             70             75             80
Tyr His Pro Asp Met Val Ala Gly Leu Ser Leu Gly Glu Tyr Ser Ala
      85             90             95
Leu Val Ala Ser Gly Ala Leu Asp Phe Glu Asp Ala Val Ala Leu Val
      100            105            110
Ala Lys Arg Gly Ala Tyr Met Glu Glu Ala Ala Pro Ala Asp Ser Gly
      115            120            125
Lys Met Val Ala Val Leu His Thr Pro
      130            135

```

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

```

Met Tyr Gln Phe Ser Gly Gln Thr Lys Val Xaa Glu Val Leu Ala Phe
 1             5             10             15
Arg Asp Lys Pro Pro Tyr Gly Gly Ser Ser Ala Met Pro Leu Arg Cys
          20             25             30
Leu

```

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

```

Met Thr Lys Glu Thr Gly Met Glu Gln Thr Phe Phe Ile Ile Lys Pro
 1             5             10             15
Asp Gly Val Lys Arg Gly Leu Val Gly Glu Val Leu Lys Arg Ile Glu
          20             25             30
Gln Arg Gly Phe Thr Ile Glu Lys Leu Glu Phe Arg Ser Gln Val Phe
          35             40             45
Arg Arg Val Asp
50

```

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

```

Met Thr Ser Gly Pro Val Leu Val Gly Val Ile Ser Gly Pro Lys Val
 1             5             10             15

```



```

Ile Glu Thr Trp Arg Thr Met Met Gly Ala Thr Arg Pro Glu Glu Ala
      20                      25                      30
Leu Pro Gly Thr Ile Arg Gly Asp Phe Ala Lys Ala Ala Gly Glu Asn
      35                      40                      45
Glu Ile Ile Gln Asn Val Val His Gly Ser Asp Ser Glu Lys Asn Gln
      50                      55                      60
Leu Ser Arg Glu Ile Ala Pro Leu Val Leu Arg Val Asp Trp Leu Asn
      65                      70                      75                      80
Gln Leu Asp Lys Ser Ser Phe Glu
                        85

```

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

```

Met Gly Leu Lys Asp Asn Ala Gly Leu Val Lys Glu Tyr Ala Leu Val
  1              5              10              15
Asp Ala Val Glu Tyr Gln Asn Val Ile Val Ala Thr Thr Val Glu Glu
      20              25              30
Met Leu Ser Lys Tyr Ala Asn Lys Asn Asp Leu Glu Ile Asp Asn Ala
      35              40              45
Thr Thr Glu Ser Ile Lys Gly Val Val Ala Asp Leu Lys Ser Ala Val
      50              55              60
Ile Lys Gly Asp Thr Val Tyr Phe Phe Lys Val Asp Gly Lys Ile Tyr
      65              70              75              80
Lys Val Lys Ala Ser Val Ser Asp Asp Leu Pro Tyr Leu Glu Asn Gly
      85              90              95
Lys Thr Phe Glu Gly Gln Val Xaa Lys Asp Asn Tyr Leu Lys Thr Phe
      100             105             110
Lys Val Gln
      115

```

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

```

Met Ile Ser Gly Ser Glu Ile Arg Asp Ile Val Thr Ser Asp Ile Pro
 1             5             10             15
Leu Ala Asp Lys Thr Glu Thr Leu Val Arg Phe Ala Asn Asn Ala Gly
      20             25             30
Gly Leu Asp Asn Ile Thr Val Ala Leu Val Ser Met Asn Glu Glu Asp
      35             40             45
Glu Glu
      50

```

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

```

Met Pro Asp Asn Leu Ala Leu Arg Met Arg Pro Lys Thr Ile Asp Gln
 1             5             10             15
Val Ile Gly Gln Glu Xaa Leu Val Gly Pro Gly Lys Ile Ile Arg Arg
      20             25             30
Met Val Glu Ala Asn Arg Leu Ser Ser Met Ile Leu Tyr Gly Pro Pro
      35             40             45
Gly Ile Gly Lys Thr Ser Ile Ala Ser Ala Ile Ala Gly Thr Thr Lys
      50             55             60
Tyr Ala Phe Arg Thr Phe Asn Ala Thr Val Asp Ser
      65             70             75

```

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

```

Met Pro Glu Glu Leu Ala Tyr Leu Val Gln His Leu Asp Asn Ala Gln
 1               5               10               15
Glu Gln Val Val Leu Gly Asn Thr Tyr His Thr Gly Asn His Cys Phe
          20               25               30
Ser

```

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

```

Met Val Phe Trp Glu Gly Leu Val Pro Thr Pro Asp Val Ile Asp Ala
 1               5               10               15
Gly His Val Thr Gly Phe Leu Tyr Thr Val His Ser Ser Ser Thr Gly
          20               25               30
Leu Ile Val Leu Gln Ile Lys Lys Asp Leu Leu Lys Leu
          35               40               45

```

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

```

Met Thr Asp Arg Tyr Asp Ser Ser Leu Gly Ile Tyr Lys Val Pro Trp
 1           5           10           15
Cys Val Ser Gln Gln Gln Thr Val Thr Glu Ile Met Asp Thr Tyr Cys
          20          25          30
Asp Trp Gly Val Lys Tyr Pro Leu Val Tyr Leu Glu Asp Pro Phe Ser
        35          40          45
Asp Glu Asp Leu Asp Ser Trp Arg Lys Phe Gln Leu Ile Lys Pro Leu
       50          55          60
Lys Leu Gln Val Phe Gly Asp Asp Phe Tyr Ala Thr Asn Leu Glu Arg
      65          70          75          80
Ile Ser Gln Phe Lys Asp Cys Ala Asp Gly Ile Val Ile Lys Pro Asn
          85          90          95
Gln Val Gly Ser Val Ser Lys Thr Leu Glu Val Met Glu Tyr Ala Glu
        100         105         110
Lys Ser Gly Ile Ser Met Ala Phe Ser Gln Arg Thr Ala Glu Thr Glu
       115         120         125
Asn Asn Ile Ile Ser His Leu Ala Met Ser Val Ile Leu Leu Ile
      130         135         140

```

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

```

Met Lys Lys Ile Ser Lys Gln Glu Leu Val Asn Thr Arg Phe Ser Arg
 1           5           10           15
Leu Phe Ala His Phe Gly Gln Glu Lys Asp Gly Ser Phe Leu Ala Gln
          20          25          30
Arg Tyr Gln Phe Tyr Leu Ala Gln Gln Gly Gln Thr Leu Ser Gly Ala
        35          40          45
His Asp Leu Leu Asp Ser Leu Ile Glu Arg Asp Tyr Asn Leu Tyr Ala
       50          55          60
Ala Thr Asn Gly Ile Thr Ala Ile Gln Thr Gly Arg Leu Ala Gln Ser
      65          70          75          80

```

Gly Leu Ala Pro Tyr Phe Asn Gln Val Phe Ile Ser Glu Gln Leu Gln
 85 90 95
 Thr Gln Lys Pro Asp Ala Leu Phe Tyr Glu Lys Ile Gly Gln Gln Ile
 100 105 110
 Ala Gly Phe Ser Lys Glu Lys Thr
 115 120

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

Met His Arg Lys Thr Val Ile Asp Xaa Arg Thr Leu Gly Glu Arg Tyr
 1 5 10 15
 Thr Phe Thr Xaa Pro Ile Lys Glu Leu Lys Thr Arg Asn Val Ala Glu
 20 25 30
 Val Ala Asp Leu Leu Ala Xaa Val Glu Ser Tyr Gln Glu Gln Asp Tyr
 35 40 45
 Tyr Val Val Gly Tyr Val Ser Tyr Glu Ala Ala Pro Ala Phe Glu Glu
 50 55 60
 Lys Leu Ala Val His Lys Val Pro Leu Leu Gly Glu Tyr Leu Leu Tyr
 65 70 75 80
 Phe Thr Val His Asp Arg Val Glu Thr Ser Pro Ile Pro Leu Thr Tyr
 85 90 95
 Glu Asp Ile Asp Leu Pro Ser Asn Trp Gln Gly Xaa Asn Val Cys Thr
 100 105 110
 Glu Leu

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

```

Met Glu Arg Ile Glu Val Arg Ser Arg Ser Gly Ser Ala His Leu Gly
 1             5             10             15
His Val Phe Thr Asp Gly Pro Arg Glu Leu Gly Gly Leu Arg Tyr Cys
          20             25             30
Ile Asn Ser Ala Ser Leu Arg Phe Val Ala Lys Asp Glu Met Glu Lys
          35             40             45
Ala Gly Tyr Gly Tyr Leu Leu Pro Tyr Leu Asn Lys
          50             55             60

```

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

```

Met Glu Trp Ile Arg Leu Ile Gly Ile Ala Ile Ile Val Val Gly Phe
 1             5             10             15
Ile Leu Lys Phe Asp Thr Ile Ala Thr Val Val Leu Ala Gly Leu Val
          20             25             30
Thr Ala Leu Val Ser Gly Val Ser Leu Val Glu Phe Leu Glu Ile Leu
          35             40             45
Gly Lys Glu Phe Ser Asn Gln Arg Val Leu Thr Ile Phe Met Val Thr
          50             55             60
Leu Pro Leu Val Gly Leu Ser Glu Thr Phe Gly Leu Asn Asn Asp Gln
          65             70             75             80
Ser Ile

```

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

```

Met Leu Leu Ile Phe Ala Val Ile Gly Val Leu Val Ala Leu Ile Ala
 1             5             10             15
Gln Phe Tyr Ser Ala Lys Ala Ala Val Gly Phe Ala Lys Glu Leu Thr
      20             25             30
Asn Asp Leu Tyr Arg His Ile Leu Ser Leu Pro Lys Asp Ser Arg Asp
      35             40             45
Arg Leu Thr Thr Ser Ser Leu Val Thr Arg Leu Thr Ser Asp Thr Tyr
      50             55             60
Gln Ile Gln Thr Gly Ile Asn Gln Phe Leu Arg Leu Phe Leu Arg Ala
65             70             75             80
Pro Ile Ile Val Phe Gly Ala Ile Phe Met Ala Tyr Arg Ile Ser Ala
      85             90             95
Glu Leu Thr Phe Trp Phe Leu Val Met Val Ala Ile Leu Thr Ile Val
      100            105            110
Ile Val Arg Val Ile Ser Ile Gly Gln Ser Ser Leu Gln
      115            120            125

```

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

```

Met Pro Ile Glu Gln Val Gln Lys Leu Leu Gly His Ser Lys Ile Asp
 1             5             10             15
Thr Thr Leu Ala Tyr Ala Met Val Asn Gln Asn Asn Val Lys His Ser
      20             25             30
His Gln Lys Phe Ile Ser
      35

```

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

```

Met Lys Pro Cys Trp Lys Lys Cys Phe Pro Glu Glu Val Ser Ser Glu
 1             5             10             15
Gly Glu Val Thr Leu Ile Glu Ile Pro Val Ser Asp Lys Ile Ala Gly
          20             25             30
Lys Gln Val His Glu Leu Asn Leu Pro His Asn Val Leu Ile Thr Thr
          35             40             45
Gln Val His Asn Gly Lys Ser Gln Thr Val Asn Gly Ser Thr Arg Met
          50             55             60
Tyr Leu Gly Asp Met Ile His Leu Val Ile Pro Lys Ser Glu Ile Gly
65             70             75             80
Lys Val Lys Asp Leu Leu Leu
          85

```

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

```

Met Asn Glu Gly Val Glu Asn Phe Arg Ala Lys Leu Ala Ser Leu Gly
 1             5             10             15
Ala Lys Asn Ile Gly Ile Tyr Val Gly Val Tyr Phe Met Glu Glu His
          20             25             30
Ser Ile Asp Thr Gly Lys Phe Thr Ser Val Trp Ile Pro Ser Tyr Gly
          35             40             45
Ser Asp Ser Gly Phe Leu Glu Ser Ser Pro Lys Thr Asp Leu Asp Tyr
50             55             60

```


Asp Ile His Gln Tyr Thr Ser Lys Gly Lys Leu Pro Ala Leu Thr Thr
 65 70 75 80
 Ile

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

Met Val Ser Lys Tyr Leu Leu Leu Ala Val Ile Phe Ser Gly Leu Val
 1 5 10 15
 Thr Trp Ile Leu Arg Met Ile Ser Phe Ile Leu Val Lys Tyr Lys Gly
 20 25 30
 Leu Pro Ala Ile Val Glu Arg Phe Leu Lys Phe Leu Pro Val Ser Ile
 35 40 45
 Ile Phe Ala Leu Ile Leu Ser Ser Val Val Thr Gly Lys Val Gly Ser
 50 55 60
 Leu Pro Gln Ile Lys Trp Leu Asp Phe Leu Ala Val Phe Pro Thr Ala
 65 70 75 80
 Trp Val Ala Phe Arg Tyr Arg Asn Leu Leu Gly Thr Val Leu Phe Gly
 85 90 95
 Val Val Leu Ile Ala Ile Leu Arg Leu Val Ser
 100 105

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

```

Met Glu Asp Xaa Glu Thr Gln Arg Val Val Met Gln Tyr Arg Ala Pro
 1              5              10              15
Glu Asn Asn Arg Trp Ser Gly Tyr Ala Phe Pro Gly Gly His Val Glu
      20              25              30
Asn Asp Glu Ala Phe Ala Glu Ser Val Ile Arg Glu Ile Tyr Glu Glu
      35              40              45
Thr Gly Leu Thr Ile Gln Asn Pro Gln Leu Val Gly Ile Lys Asn Trp
      50              55              60
Pro Leu Asp Thr Gly Gly Arg Tyr Ile Val Ile Cys Tyr Lys Ala Thr
65              70              75              80
Glu Phe Ser Gly Thr Leu Gln Ser Ser Glu Glu Gly Glu Val Ser Trp
      85              90              95
Val Gln Lys Asp Gln Ile Pro Asn Leu Asn Leu Ala Tyr Asp Met Leu
      100              105              110
Pro Leu Met Glu Met Met Glu Ala Pro Asp Lys Ser Glu Phe Phe Tyr
      115              120              125
Pro Arg Arg Thr Glu Asp Asp Trp Glu Lys Lys Ile Phe
      130              135              140

```

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

```

Met Thr Ile Glu Leu Leu Thr Pro Phe Thr Lys Val Glu Leu Glu Pro
 1              5              10              15
Glu Ile Lys Glu Lys Lys Arg Lys Gln Val Gly Ile Leu Gly Gly Asn
      20              25              30
Phe Asn Pro Val His Asn Ala His Leu Ile Val Ala Asp Gln Val Arg
      35              40              45
Gln Gln Leu Gly Leu Asp Gln Val Leu Leu Met Pro Glu Tyr Gln Pro
      50              55              60
Pro His Val
65

```

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

```

Met Lys Lys Leu Val Phe Val Cys Leu Gly Asn Ile Cys Arg Ser Pro
 1             5             10             15
Met Ala Glu Phe Val Met Lys Ser Met Thr Asp Asn Tyr Glu Ile Gln
          20             25             30
Ser Arg Ala Thr Ser Ser Trp Glu His Gly Asn Pro Ile His Lys Gly
          35             40             45
Thr Gln Gly Ile Phe Gln Glu Tyr Glu Ile Pro Tyr Asp Lys Asn Lys
          50             55             60
Thr Ser Leu Gln Ile Ser Lys Glu Asp Phe Glu Ala Phe Asp Tyr Ile
          65             70             75             80
Ile Gly Met Asp Ala Ser Asn Val Pro Thr Tyr Val Arg Cys Val Gln
          85             90             95

```

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

```

Met Val Lys Tyr Gly Val Val Gly Ala Gly Tyr Phe Gly Ala Glu Leu
 1             5             10             15
Ala Arg Tyr Met Gln Lys Asn Asp Gly Ala Xaa Ile Thr Leu Leu Tyr
          20             25             30
Asp Pro Asp Asn Ala Glu Ala Ile Ala Glu Glu Leu Gly Ala Lys Val
          35             40             45
Ser Lys Phe Leu Arg
          50

```

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

```

Met Leu Trp Lys Tyr Tyr Asn Ser Ser Phe Leu Lys Ala Val Pro His
 1             5             10             15
Leu Thr Thr Glu Tyr Lys Arg Leu Ala Gln Ala His Gly Leu Asn Leu
          20             25             30
Lys Gln Ala Lys Pro Ile Thr Met Gly Met Trp Ile Gly Gly Asp Arg
          35             40             45
Glu Gly Asn Pro Phe Val Thr Ala Lys Asn Leu Lys Gln Ser Ala Leu
          50             55             60
Thr Gln Cys Glu Val Xaa Leu Asn Leu Leu
65             70

```

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

```

Met Asn Thr Leu Tyr Leu Asn Gln His Ser Ser Tyr Lys Asn Asp Glu
 1             5             10             15
Asp Ser His Ser Phe Pro Ile Gln Met Glu Leu Val Ser Asp Glu Met
          20             25             30
Ile Pro Arg Asn
          35

```

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

```

Met Ala Arg Lys Glu Thr Met Ala Glu Arg Lys Tyr Cys Lys Met Lys
 1           5           10           15
Lys Asp Ile His Pro Glu Tyr Arg Pro Val Val Phe Met Asp Thr Thr
          20           25           30
Thr Gly Tyr Gln Phe Leu Ser Gly Ser Thr Lys Arg Ser Asn Glu Thr
          35           40           45
Val Glu Phe Glu Gly Glu Thr Tyr Pro Leu Ile Arg Val Glu Ile Ser
          50           55           60
Ser Asp Ser His Pro Phe Tyr Thr Gly Arg Gln Lys Phe Thr Gln Ala
65           70           75           80
Asp Gly Arg Val Asp Arg Phe Asn Lys Lys Tyr Gly Leu Lys
          85           90

```

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

```

Met Glu Thr Ala Leu Ile Ser Val Ile Val Pro Val Tyr Asn Val Ala
 1           5           10           15
Gln Tyr Leu Glu Lys Ser Ile Ala Ser Ile Gln Lys Gln Thr Tyr Gln
          20           25           30
Asn Leu Glu Ile Ile Leu Val Asp Asp Gly Ala Thr Asp Glu Ser Gly
          35           40           45
Arg Leu Cys Asp Ser Ile Ala Glu Gln Asp Asp Arg Val Ser Val Leu
          50           55           60

```

His Lys Lys Asn Glu Gly Leu Ser Gln Ala Arg Asn Asp Gly Met Lys
 65 70 75 80
 Pro Gly Ser Arg Gly Leu Ser Asp Phe Tyr
 85 90

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

Met Tyr Phe Leu Ile Asn Phe Val Tyr Pro Val Asp Met Val Ile Asn
 1 5 10 15
 Leu Pro Phe Leu Ile Asn Thr Gly Leu Ile Val Leu Leu Ser Ala Ile
 20 25 30
 Ser Tyr Ile Ser Leu Leu Val Phe Thr Lys Asp Ser Ile Phe Tyr Glu
 35 40 45
 Phe Leu Asn His Val Leu Ala Leu Lys Asn Lys Phe Lys Lys Ser
 50 55 60

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

Met Arg Val Ile Ala Trp Leu Glu Pro Ser Arg Lys Ile Leu Gln Pro
 1 5 10 15
 Gly Ala Asn Asp Val Trp Val Val Lys Arg Lys Gly Lys Arg Asp Leu
 20 25 30
 Leu Leu Pro Tyr Ile Pro Pro Val Val Leu Asn Val Asp Ile Pro Asn
 35 40 45

Lys Arg Val Asp Val Glu Ile Leu Glu Gly Leu Asp Asp Glu Asp
 50 55 60

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

Met Asp Asp Asp Phe Lys Arg Tyr Asn Ala Pro Ile Leu Thr Trp Tyr
 1 5 10 15
 Glu Thr Ala Arg Tyr Ala Phe Glu Arg Gly Met Val Trp Gln Asn Leu
 20 25 30
 Gly Gly Val Glu Asn Ser Leu Asn Gly Gly Leu Tyr His Phe Lys Glu
 35 40 45
 Lys Phe Asn Pro Thr Ile Glu Glu Tyr Leu Gly Glu Phe Thr Met Pro
 50 55 60
 Thr His Pro Leu Tyr Pro Leu Leu Arg Leu Ala Leu Asp Phe Arg Lys
 65 70 75 80
 Thr Leu Arg Lys Lys His Arg Lys
 85

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

Met Glu Asp Phe Phe Ala Trp Cys Arg Arg Gln Ser Val Leu Ser Gly
 1 5 10 15
 Ser Lys Leu Gly Arg Ala Ile Glu Tyr Ser Leu Lys Tyr Glu Glu Thr
 20 25 30

Phe Lys Thr Ile Leu Lys Asp Gly His Leu Val Leu Ser Asn Asn Leu
 35 40 45
 Ala Glu Arg Ala Ile Lys Ser Leu Val Met Gly Arg Ser Lys Arg Val
 50 55 60
 Gln Trp Thr Leu Leu Ala
 65 70

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

Met Thr Lys Gln Gly Ser Trp Lys Leu Ile Leu Glu Asp Glu Ser Ala
 1 5 10 15
 Gly Arg Glu Leu Phe Pro Ile Leu Thr Gln Gly Xaa Tyr Ile Ala Thr
 20 25 30
 Phe Asp Gln Gln Ala Pro Xaa Ile Asp Glu Ile Phe Lys Leu
 35 40 45

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

Met Thr Thr Asn Xaa Asp Asn Asp Thr Ser Glu Arg Ser Asp Cys Tyr
 1 5 10 15
 Arg Lys Arg Thr Ala Gly Glu Thr Pro Met Asn Asp Leu Thr Ser His
 20 25 30
 Thr His Gly Gly Asn Tyr Thr Ile Ala Arg Tyr Gln Glu Lys Phe
 35 40 45

Trp Asn Lys Gln Leu

50

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

```

Met Ala Gln His Ala Ala Val Glu Ala Leu Thr Ala Gly Lys Asn Asp
 1             5             10             15
Ala Glu Pro Met Lys Lys Glu Tyr Ile Gln Arg Arg Asp Tyr Ile Ile
          20             25             30
Glu Lys Met Thr Ala Leu Gly Phe Glu Ile Ile Lys Pro Asp Gly Ala
          35             40             45
Phe Tyr Ile Phe Ala Lys Ile Pro Ala Gly Tyr Asn Gln Asp Ser Phe
          50             55             60
Ala Phe Leu Lys Asp Phe Ala Gln Lys Lys Ala Val Ala Phe Ile Pro
65             70             75             80
Gly Ala Ala Phe Gly Arg Tyr Gly Glu Gly Tyr Val Arg Leu Ser Tyr
          85             90             95
Ala Ala Ser Met Glu Thr Ile Lys Glu Ala Met Lys Arg Leu Glu Glu
          100             105             110
Tyr Met Arg Glu Ala
          115

```

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

```

Met Asn Ile Thr Asn Leu Phe Ser Ile Lys Thr Gly Cys Asp Glu Thr
 1             5             10             15
Asp Arg Gln Leu Gln Lys Leu Phe Phe Gln Leu Asp Leu Gln Leu Gly
          20             25             30
Glu Leu Thr Asp Gln Leu Arg Lys Leu Asp Ser Asn Phe Val Pro Arg
          35             40             45
Ser Gln Phe Val Asp Thr Leu Asp Leu Asn Asp Val Glu Tyr Lys Glu
          50             55             60
Ile Leu Asn Tyr Phe Ile Phe His Arg Asn Asp Ser Glu Glu Ser Leu
65             70             75             80
Val Glu Trp Leu Tyr Asp Trp Ile Ser Thr Asn Arg Tyr Glu Leu Pro
          85             90             95

```

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

```

Met Leu Gln Trp Ile Asp Arg Thr Phe Gln Asp Tyr Leu Glu Leu Glu
 1             5             10             15
His Leu Val Leu Thr Thr Trp Ser Gly Asn Leu Gly Met Met Lys Leu
          20             25             30
Ala Glu Lys Leu Xaa Met Lys Lys Xaa Ala His Ile Xaa Lys Val Arg
          35             40             45
Tyr Tyr Gln Gly Lys Tyr Phe Asp Ser Ile Lys Tyr Gly Ile Leu Arg
          50             55             60
Xaa Asp Trp Glu Lys Ile Asn Asp Gly Tyr Tyr Gln Ile Tyr Xaa Asn
65             70             75             80
Ser

```

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

```

Met Ile Val Glu Glu Val Arg Asp Arg Tyr Val Gly Lys Val Asp Ala
 1           5           10           15
Val Phe His Asn Gly Asp Ser Glu Leu Arg Pro Asp Ser Pro Leu Trp
          20           25           30
Glu Gly Ile Arg Val Val Lys Gly Asn Met Asp Phe Tyr Ala Gly Tyr
          35           40           45
Pro Glu Arg Leu Val Thr Glu Leu Gly Ser Thr Lys Ile Ile Gln Thr
          50           55           60
His Gly His Leu Phe Asp Ile Asn Phe Asn Phe Gln Lys Leu Asp Tyr
65           70           75           80
Trp Ala Gln Glu Glu Glu Ala Ala Ile Cys Leu Tyr Gly His Leu His
          85           90           95
Val Pro Ser Ala Trp Leu Glu Gly Lys Ile Leu Phe Leu Asn Pro Gly
          100          105          110
Ser Ile Ser Gln Pro Arg Gly Thr Ile Arg Glu Cys Leu Tyr Ala Arg
          115          120          125
Val Glu Ile Asp Asp Ser Tyr Phe Lys Val Asp Phe Leu Thr Arg Asp
          130          135          140
His Glu Val Tyr Pro Gly Cys Pro Arg Ser Leu Ala Asp Asp Ala Lys
145          150          155          160
Glu Leu Arg Leu Ser Val Gly Ala Glu Asn Phe
          165          170

```

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

```

Met Asn Leu His Gln Pro Leu His Val Leu Pro Gly Val Gly Pro Lys
 1           5           10           15

```

Ser Ala Glu Lys Tyr Ala Lys Leu Gly Ile Glu Asn Leu Gln Asp Leu
 20 25 30
 Leu Leu Tyr Phe Pro Phe Arg Tyr Glu Asp Phe Lys Thr Lys Gln Val
 35 40 45
 Leu Glu Leu Glu Asp Gly Glu Lys Ala Val Leu Ser Gly Gln Val Val
 50 55 60
 Thr Pro Ala Ser Val Gln Tyr Tyr Gly Phe Gln Ala Ala Asn Pro Pro
 65 70 75 80
 Ala Phe Leu Val Leu Gln Ala Arg Glu Glu Gly Ser Phe Phe Phe Gly
 85 90 95
 Gly

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

Met Gln Leu Leu Ser Glu Asn Met Leu Lys Thr Ile Gln Ser Leu Ser
 1 5 10 15
 Val Trp Gln Ile Tyr Leu Leu Gly Phe Glu Arg Ile Leu Ala Leu Gly
 20 25 30
 Phe Gln Leu Leu Thr Val Trp Val Tyr Gln Ala Val Arg Gln Lys
 35 40 45
 Lys Trp Ile Tyr Leu Leu Ala Ala Tyr Gly Leu His Ala Phe Phe Asp
 50 55 60
 Leu Ala Pro Ser Leu Phe Gln Val Gly Trp Leu Thr Asn Pro Val Leu
 65 70 75 80
 Val Glu Val Ile Leu Ala Leu Glu Leu Val Leu Val Ala Tyr Gly Thr
 85 90 95
 Lys Glu Ile Phe Cys Lys Lys Ser
 100

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

```

Met Thr Lys Ser Met Thr Pro Asp Arg Glu Val Ile Thr Phe Ile Pro
 1           5           10           15
Glu Lys Phe Ile Val Asp Gly Phe Gln Gly Ile Arg Asp Pro Arg Gly
          20           25           30
Met Met Gly Val Arg Leu Glu Met Arg Gly Leu Leu Tyr Thr Gly Pro
          35           40           45
Arg Thr Ile Leu His Asn Leu Arg Lys Thr Val Glu Arg Ala Gly Val
          50           55           60
Gln Val Glu Asn Val Ile Ile Ser Pro Leu Ala Met Val Gln Ser Val
          65           70           75           80
Leu Asn Glu Gly Glu Arg Glu Phe Gly Ala Thr Val Ile Asp Met Gly
          85           90           95
Ala Gly Gln Thr Thr Val Ala Thr Ile Arg Asn Gln Glu Leu Gln Phe
          100          105          110
Thr His Ile Leu Gln Glu Val Glu Ile Met
          115          120

```

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

```

Met Leu Asn Ser Ile Val Thr Ile Ile Cys Ile Ala Leu Ile Ala Phe
 1           5           10           15
Ile Leu Phe Trp Phe Phe Lys Lys Pro Glu Lys Ser Gly Gln Lys Ala
          20           25           30
Gln Gln Lys Asn Gly Tyr Gln Glu Ile Arg Val Glu Val Met Gly Gly
          35           40           45

```

Tyr Thr Pro Glu Leu Ile Val Leu Lys Lys Ser Val Pro Ala Arg Ile
 50 55 60
 Val Phe Asp Arg Lys Asp Pro Ser Pro Cys Leu Asp Gln Ile Val Phe
 65 70 75 80
 Pro Asp Phe Gly Val His Ala Asn Leu Pro Met Gly Glu Glu Tyr Val
 85 90 95
 Val Glu Ile Thr Pro Glu Gln Ala Gly Glu Phe Gly Phe Ala Cys Gly
 100 105 110
 Met Asn Met Met His Gly Lys Met Ile Val Glu
 115 120

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

Met Lys Ile Val Ser Gly Ile Tyr Gly Gly Arg Pro Leu Lys Thr Leu
 1 5 10 15
 Glu Gly Lys Thr Thr Arg Pro Thr Ser Asp Lys Val Arg Gly Ala Ile
 20 25 30
 Phe Asn Met Ile Gly Pro Tyr Phe Glu Val Gly Xaa Val Leu Asp Leu
 35 40 45
 Tyr Ala Gly Ser Gly Gly Leu Ser Ile Glu Ala Val Ser Arg Gly Met
 50 55 60
 Ser Ser Ala Val Leu Val Glu Arg Asp Arg Lys Ala Gln Thr Ile Val
 65 70 75 80
 Ala Glu Asn Ile Gln Met Thr Lys Glu Val Gly Lys Phe Gln Leu Leu
 85 90 95
 Gln Asn Gly Cys Arg Lys Gly Ile Gly Thr Gly Xaa Leu Gly Asn Leu
 100 105 110
 Thr Ser Phe Ser
 115

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

```

Met Xaa Thr Asn Phe Thr Asp Gln Val Asp Thr Met Ile Tyr Val Asp
 1             5             10             15
Lys Glu Glu Lys Glu Thr Ile Lys Ala Ala Leu Val Glu Phe Phe Asn
          20             25             30
Gly Lys Val Thr Leu Thr Asp Gln Gly Leu Arg Glu Val Glu Val Pro
          35             40             45
Val Asn Leu Val
          50
  
```

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

```

Met Ile Gly Val Ala Leu Glu Glu Ser Pro Thr Leu Lys Ile His His
 1             5             10             15
Leu Thr His Asp Ile Thr Pro Tyr Asn Ile Phe Glu Gly Ser Tyr Arg
          20             25             30
Leu Phe Gln Thr Val Asp Tyr Trp Pro Glu Gly Thr Thr Phe Val Ser
          35             40             45
Val Val Asp Pro Gly Val Gly Ser Lys Arg Lys Ser Val Val Ala Lys
          50             55             60
Thr Ala Gln Lys Ser Ile His Cys His Ala Arg
65             70             75
  
```

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

```

Met Glu Leu Arg Arg Pro Arg Leu Ala Asp Lys Lys Ala Val Leu Asp
 1             5             10             15
Met Met Thr Glu Phe Glu Lys Ser Gln Ser Ala His Asp Gly Gly Phe
          20             25             30
Trp Asp Thr Glu Asn Phe Val Tyr Glu Glu Trp Leu Glu Ser Asn Gln
          35             40             45
Glu Gln Glu Met Gly Ile Asn Leu Pro Glu Gly Trp Val Pro Ala Ile
 50             55             60
Gln Leu Val Ala Phe Ser Glu Lys Gly Gln Ala Val Gly Phe Leu Asn
65             70             75             80
Leu Arg Leu Arg Leu Ser Asn Phe Leu Leu Glu Glu Gly Gly His Ile
          85             90             95
Gly Tyr Ser Ile Arg Pro Ser Glu Arg Gly Lys Gly Tyr Ala Lys Glu
          100            105            110
Leu Ser Val Arg Ala Cys Lys Leu Leu Arg Lys Arg Thr Ser Arg Lys
          115            120            125
Leu Trp
          130
  
```

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

```

Met Thr Phe Ile Arg Gly Pro Ile Ile Ser Thr Val Gly Glu Gly Val
 1             5             10             15
Xaa Ile Leu Ala Thr Val Asn Xaa Gln Phe Val Xaa Xaa Gln Xaa Xaa
          20             25             30
  
```


Asn Met Leu Val Ser Pro Phe His Pro Glu Leu Thr Asp Xaa Xaa Arg
 35 40 45
 Leu Xaa Gln Tyr Phe Ile Ser Met Cys Lys Glu Lys Ser Xaa Asp
 50 55 60

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

Met Lys Gly Asp Val Ile Thr Glu His Gln Phe Tyr Glu Gln Val Lys
 1 5 10 15
 Asn Asn Pro Ser Ala Gln Xaa Val Leu Leu Asn Met Thr Ile Gln Lys
 20 25 30
 Val Phe Glu Lys Thr Ile Trp Leu Arg Ala
 35 40

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

Met Asp Lys Ala Leu Ala Asp Leu Lys Thr Ser Gly His Leu Pro Ile
 1 5 10 15
 Pro Arg His Leu Arg Asp Gly His Tyr Xaa Gly Ser Lys Glu Leu Gly
 20 25 30
 Asn Ala Gln Asp Tyr Leu Tyr Pro His Asn Tyr Pro Xaa Asn Trp Val
 35 40 45
 Lys Gln Asp Tyr Leu Pro Gln Lys Ile Arg Asn His His Tyr Phe Gln
 50 55 60

Ala Glu Tyr Thr Gly Lys Tyr Glu Arg Ala Leu Ala Gln Arg Lys Glu
 65 70 75 80
 Ala Ile Asp His Leu Arg Lys Ile
 85

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

Met Val Val Phe Thr Gly Ser Thr Val Glu Glu Ala Ile Gln Lys Gly
 1 5 10 15
 Leu Lys Glu Leu Asp Ile Pro Arg Met Lys Ala His Ile Lys Val Ile
 20 25 30
 Ser Arg Glu Lys Lys Gly Phe Leu Gly Leu Phe Gly Lys Lys Pro Ala
 35 40 45
 Gln Val Asp Ile Glu Ala Ile Ser Glu Thr Thr Val Val Lys Ala Asn
 50 55 60
 Gln Gln Val Val Lys Gly Val Pro Lys Lys Ile Asn Asp Leu Asn Glu
 65 70 75 80
 Pro Val Lys Thr Val Ser Val Arg Asn Arg
 85 90

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

Met Thr Lys Arg Cys Ser Trp Val Lys Met Thr Asn Pro Leu Tyr Ile
 1 5 10 15

Ala Tyr His Asp Glu Glu Trp Gly Gln Pro Leu His Asp Asp Gln Ala
 20 25 30
 Leu Phe Glu Leu Leu Cys Met Glu Thr Tyr Gln Ala Gly Leu Ser Trp
 35 40 45
 Glu Thr Val Leu Asn Lys Arg Gln Ala Phe Arg Glu Ala Phe Pro
 50 55 60

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

Met Phe Val Gly Gln Glu Trp Thr Asn Gln Thr Phe Val Asp Leu Leu
 1 5 10 15
 Gly Asn His Gln Gly Gln Val Thr Ile Asp Glu Glu Gly Tyr Gly Gln
 20 25 30
 Phe Pro Val Ser Ala Arg Ser Val Ser Val Trp Ala Val Asn Thr Ile
 35 40 45

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

Met Ala Gln Val Asp Ile Ile His Gly Ile Gly Thr Gly Val Ile Arg
 1 5 10 15
 Glu Gly Val Thr Lys Tyr Leu Gln Arg Asn Lys His Val Lys Ser Phe
 20 25 30
 Gly Tyr Ala Pro Gln Asn Ala Gly Gly Ser Gly Ala Thr Ile Val Thr
 35 40 45

Phe Lys Gly

50

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

```

Met Asn Leu Leu Glu Glu Ala Thr Lys Gly Lys Val Ile Phe Glu Gly
 1             5             10             15
Val Asp Ile Thr Asp Lys Lys Asn Asp Leu Phe Pro Met Arg Glu Lys
             20             25             30
Met Gly Met Val Phe Gln Gln Phe Asn Xaa Phe Leu Ile
             35             40             45

```

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

```

Met Gln Ile Asp Leu Ala Asn Leu Leu Pro Asp Leu Pro Gly Asn Leu
 1             5             10             15
Ser Gly Ile Asn Pro Asn Arg Tyr Val Phe Tyr Gln Asp Val Leu Cys
             20             25             30
Pro Ile Leu Asp Arg His Met Thr Pro Glu Gln Asp Lys Pro His Phe
             35             40             45
Ala Gln Ala Ala Gly Thr Ile Ala Asp Ile Lys Glu Lys Ala Gly Asn
             50             55             60
Tyr Ala Tyr Leu Phe Glu Thr Gln Ala Gln Leu Asn Ala Ile Leu Ser
65             70             75             80

```

Ser Lys Val Asp Val Gly Arg Arg Ile Arg His Ala Tyr Gln Ala Asp
 85 90 95
 Asp Lys Glu Ser Leu Gln Gln Ile Ala Arg Gln Glu Leu Pro Glu Leu
 100 105 110
 Arg Ser Gln Ile Glu Asp Phe His Ala Leu Phe Ser His His Trp Leu
 115 120 125
 Lys

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

Met Arg Gln Gly Ile Asp Ser Leu Ala Tyr Val Val Lys Thr His Phe
 1 5 10 15
 Glu Leu Asp Pro Phe Ser Gly Gln Ala Phe Leu Phe Cys Gly Gly Arg
 20 25 30
 Lys Asp Arg Phe Lys Ala Leu Tyr Trp Asp Gly Gln Gly Phe Trp Leu
 35 40 45
 Leu Tyr Lys Arg Phe Glu Asn Gly Lys Leu Thr
 50 55

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

Met Asn Ala Phe Leu Glu Glu Leu Ser Gln Ala Tyr Pro Asp Asp Tyr
 1 5 10 15

```

Phe Leu Leu Val Met Asp Asn Ala Ile Trp His Lys Ser Ser Val Leu
      20                      25                      30
Lys Ile Pro Thr Asn Ile Gly Phe Ala Phe Ile Pro Pro Tyr Thr Pro
      35                      40                      45
Glu Met Asn Pro Ile Glu Gln Val Trp Lys Glu Ile Arg Lys Arg Gly
      50                      55                      60
Phe Lys Asn Lys Ala Phe Arg Ile Leu Glu Asp Val Met Asn Gln Leu
      65                      70                      75                      80
Gln Asp Val Ile Gln Gly Leu Glu Lys Glu Val Ile Lys Ser Ile Val
      85                      90                      95
Asn Arg Arg Trp Thr Arg Met Leu Phe Glu Ser Arg
      100                      105

```

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

```

Met Thr Val Glu Glu Glu Lys Val Phe Leu Ala Arg His Leu Lys Ala
  1                      5                      10                      15
Thr Glu Ala Gly Glu Phe Val Thr Ile Asp Ala Leu Phe Gln Ala Tyr
      20                      25                      30
Lys Lys Glu Leu Gly Arg Ser Tyr Thr Arg Asp Ala Phe Tyr Gln Leu
      35                      40                      45
Leu Lys Arg His Gly Trp Arg Asn Ile Met Pro Arg Pro Glu His Pro
      50                      55                      60
Lys Lys Ala Asp Ala Gln Thr Ile Val Ala Ser Lys Asn Lys Ile Ser
      65                      70                      75                      80
Ile Gln Glu Asp Lys Lys Ala Ile
      85

```

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

```

Met Leu Ser Leu Val Val Leu Ile Thr Gln Tyr Ala Thr His Gly Glu
 1           5           10           15
Leu Phe Glu Asn Tyr Ile Ser Lys Glu Asn Asp Asn Val Ile Lys Glu
          20           25           30
Tyr Gln Asn Thr Thr Gly Phe Ser Thr Pro Tyr Thr Leu Asp Gly Ser
          35           40           45
Val Leu Ile Val His Pro Asp Leu Thr Lys Gly Met Asn Ile Glu Gly
          50           55           60
Tyr Ser Asp Leu Leu Lys Pro Glu Leu Lys Gly Lys Ile Ala Thr Ala
65           70           75           80
Asp Pro Ala Asn Ser Ser Ser Ala Phe Ala Gln Leu Thr Asn Met Leu
          85           90           95
Gln Ala Gln Gly Gly Tyr Lys Asp Asp Leu Ala Trp Ser Val Leu Ser
          100          105          110
Thr Ile Phe Ser Thr Leu Ile Asp Gly Ile Val Lys
          115          120

```

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

```

Met Leu Ala Arg Lys Asp Arg Phe Tyr Tyr Ile Asp Lys Ala Thr Gly
 1           5           10           15
Lys Ala Leu Gly Ile Phe Leu Ser Cys Val Leu Thr Ser Asn Gly Val
          20           25           30
Ile Glu Val Gly Ala Val Thr Phe Ser Pro Lys Leu Arg Gly Thr Arg
          35           40           45

```

Ile Gly Thr Glu Ala Gln Tyr Leu Leu Ala Arg Tyr Val Phe Glu Glu
 50 55 60
 Leu Asn Tyr Arg Arg Tyr Glu Trp Lys Cys Asp Ala Leu Asn Leu Pro
 65 70 75 80
 Ser Arg Arg Ala Ala Glu Arg Leu Gly Phe Ile Tyr Glu Gly Thr Phe
 85 90 95
 Arg Gln Ala Val Val Tyr Lys Gly Arg Thr Arg Asp Met Asp Trp Leu
 100 105 110
 Ser Met Ile Asp Lys Asp Trp Pro Lys Val Lys Asp Arg Leu Glu Thr
 115 120 125
 Trp Leu Arg Pro Glu Asn Phe Asp Lys Asn Gly Gln Gln Tyr Lys Ser
 130 135 140
 Leu Arg Glu Leu
 145

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

Met Met Thr Ser Asp Phe Phe Glu Val Trp Phe Gln Lys Phe Leu Leu
 1 5 10 15
 Pro Thr Leu Thr Thr Pro Ser Val Ile Ile Val Lys
 20 25

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

Met	Val	Ser	Thr	Lys	Thr	Gln	Ile	Ala	Gly	Phe	Glu	Phe	Asp	Asn	Cys
1				5					10					15	
Leu	Met	Asn	Ala	Ala	Gly	Val	Ala	Cys	Met	Thr	Ile	Glu	Glu	Leu	Glu
			20					25						30	
Glu	Val	Lys	Asn	Ser	Ala	Ala	Gly	Thr	Phe	Val	Thr	Lys	Thr	Ala	Thr
		35					40					45			
Leu	Asp	Phe	Arg	Gln	Gly	Asn	Pro	Glu	Pro	Arg	Tyr	Gln	Asp	Val	Pro
	50					55					60				
Leu	Gly	Ser	Ile	Asn	Ser	Met	Gly	Leu	Pro	Asn	Asn	Gly	Leu	Asp	Tyr
65					70					75				80	
Tyr	Leu	Asp	Tyr	Leu	Leu	Asp	Leu	Gln	Glu	Lys	Glu	Ser	Asn	Arg	Thr
			85						90					95	
Phe	Phe	Leu	Ser	Leu	Val	Gly	Met	Ser	Pro	Glu	Lys	Pro	Ile	Leu	Phe
			100					105						110	

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

Met	Thr	Tyr	Leu	Met	Phe	Ser	Gly	Leu	Asp	Glu	Asn	Phe	Tyr	His	Phe
1				5				10					15		
Pro	Trp	Glu	Val	Phe	Ala	Gly	Phe	Gly	Ile	Ile	Phe	Leu	Ala	Cys	Pro
			20					25					30		
Glu	Lys	Val													
		35													

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

```

Met Phe Thr Gly Trp Phe Ala Gln Thr Phe Leu His Gln Phe Ile Arg
 1             5             10             15
Gly Ala Trp Gly Leu Gly Phe Met Ile Phe Ile Ala Phe Pro Met Gly
             20             25             30
Lys Glu Leu Leu Glu Gly Glu Tyr His Glu His Asp
             35             40

```

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

```

Met Gln Glu Lys Ile Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Thr
 1             5             10             15
His Thr Val Ile Glu Leu Ile Gln Ala Gly His Gln Val Val Val Val
             20             25             30
Asp Asn Leu Val Asn Ser Asn Xaa Lys Ser Leu Glu Val Val Glu Arg
             35             40             45
Ile Thr Gly Val Glu Ile Pro Phe Tyr Glu Ala Asp Ile Xaa Asp Thr
             50             55             60
Asp Thr Leu Arg Asp Ile Phe Lys Gln Glu Glu Leu Thr Gly Val Ile
             65             70             75             80
His Phe Ala Gly Leu Lys Ala Val Gly Glu Ser Thr Arg Ile Pro Leu
             85             90             95
Ala Tyr Tyr Asp Asn Asn Ile Ala Gly Thr Val Ser Leu Leu Lys Ala
             100            105            110
Met Glu Glu Asn Asn Cys Lys Asn Ile Ile Phe Ser Ser Xaa Ala Thr
             115            120            125
Val Tyr Gly Asp Pro Tyr Thr Val Pro Ile Leu Glu Val Ser His Phe
             130            135            140
Gln
145

```

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

```

Met Val Lys Glu Lys Val Thr Leu Thr Pro Leu Ala Ser Gly Tyr Gln
 1             5             10             15
Ile Gly Glu Glu Glu Phe Glu Gln Val Ile Leu Ala Xaa Gly Ala Trp
          20             25             30
Leu Gly Asp Met Leu Glu Pro Leu Gly Tyr Glu Val Asp Val Arg Pro
      35             40             45
Gln Lys Gly Gln Leu Arg Asp Tyr Gln Leu Val Gln Asp Met Glu Ala
 50             55             60
Tyr Pro Val Val Met Pro Glu Gly Glu Trp Asp Leu Ile Pro Phe Ala
65             70             75             80
Gly Gly Lys Leu Ser Leu Gly Ala Thr His Glu Asn Asp Met Gly Phe
          85             90             95
Asp Leu Thr Val Asp Glu Thr Leu Leu Gln Gln Met Glu Glu Ala Thr
      100             105             110
Leu Thr His Tyr Leu Ile Leu Ala Glu Ala Thr Ser Lys Ser Glu Arg
      115             120             125
Val Gly Ile Arg Ala Tyr Thr Ser Asp Phe Ser Pro Phe Phe Gly Gln
      130             135             140
Val Pro Asp Leu Thr Gly Val Tyr Ala Ala Ser Gly Leu Gly Ser Ser
145             150             155             160
Gly Leu Thr Thr Gly Pro Ile Ile Gly Tyr His Leu Ala Gln Leu Ile
          165             170             175
Gln Asp Lys Glu Leu Thr Leu Asp Pro Glu Asn Tyr Pro Ile Glu Asn
      180             185             190
Tyr Val Lys Arg Val Lys Ser Glu
      195             200

```

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

```

Met Glu His Ile Ile Tyr Gln Phe Glu Glu Asp Leu Ala Ile Leu Thr
 1             5             10             15
Leu Asn Arg Pro Glu Val Ala Asn Gly Phe His Ile Pro Met Cys Glu
             20             25             30
Glu Ile Leu Glu Ala Leu Thr Leu Ala Glu Glu Asn Pro Ala Val His
             35             40             45
Phe Ile Leu Ile Asn Ala Asn Gly Lys Val Phe Ser Val Gly Gly Asp
             50             55             60
Leu Val Glu Met Lys Arg Ala Val Asp Glu Asp Asp Ile Pro Ser Leu
65             70             75             80
Thr Lys Ile Ala Glu Leu Val Asn Thr Ile Ser Tyr Lys Ile Lys Gln
             85             90             95
Ile Ala Lys Pro Val Phe Asn Gly Ser
             100             105

```

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

```

Met Gln Pro Glu Val Ile Trp Leu Gln Lys Ile Ala Lys Pro Ser Gln
 1             5             10             15
Met Lys Val Leu Asn Thr Thr Asp Arg Val Gln Ala Ile Lys Asp Asp
             20             25             30
Val Asp Ile Ile Gln Asn Ser Leu Gln Ile Ile Asn Gln Gln Lys Glu
             35             40             45
Leu Ile Lys Glu Tyr Gln Glu Asp Leu Thr Tyr Lys Phe Lys Val Leu
             50             55             60
Glu Lys Asp Ile Gln Thr Arg Thr Ser Cys Asp Lys Arg Asn Ala Gly
65             70             75             80
Asn

```

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

```

Met Gly Ser Asn Ser Leu Thr Leu Leu Leu Lys Ile Gln Ala Thr Ile
 1             5             10             15
Pro Arg Asn Ile Tyr Asp Asn Leu Gln Ala Gly Ser Lys Val Thr Leu
          20             25             30
Asp Arg Ala Tyr Gly His Met Ile Ile Glu Glu Gly Arg Glu Asn Gln
          35             40             45
Val Trp Ile Ala Gly Gly Ile Gly Ile Thr Pro Phe Ile Ser Tyr Ile
          50             55             60
Arg Glu His Pro Ile Leu Asp Lys Gln Val His Phe Tyr Tyr Ser Phe
          65             70             75             80
Arg Gly Asp Glu Asn Ala Val Tyr Leu Asp Leu Leu Arg Asn Tyr Ala
          85             90             95
Gln Lys Asn Pro Asn Phe Glu Leu His Leu Ile Asp Ser Thr Lys Asp
          100            105            110
Gly Tyr Leu Asn Phe Glu Gln Lys Lys Cys Pro Asn Met Gln Pro Ser
          115            120            125
Ile Cys Val Val Leu Phe Leu
          130            135

```

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

```

Met Phe Phe Val Leu Ala Tyr Ala Lys Ala Val Ala Gly Arg Asn Ile
 1           5           10           15
Lys Leu His Pro Ile Gln Arg Gln Gly Ala Gly Tyr His Ser Val Asn
 20           25           30
Lys Asp Val Asp Phe Ala Ser Ala Thr Ala Leu Arg Gln His Gln Lys
 35           40           45
Asp Gln Asp Phe Leu Glu Arg Phe Met Pro Ser Val Ala Leu Phe Glu
 50           55           60
Gln Ala Ser Lys Val Ile Trp Glu Asp Tyr Phe Pro Leu Leu Arg Tyr
 65           70           75           80
Gln Ile Leu Ser Asn Pro Asp Leu Thr Thr Ile Tyr Gln Val Asn Gln
 85           90           95
Glu Met Ala Val Arg Ile Lys Glu Ala Ile Lys Thr Ala Gln Ser Val
 100          105          110
Glu Glu Leu Val Glu Leu Val Thr Thr Lys Arg Tyr Thr Lys Ala Arg
 115          120          125
Val Arg Arg Leu Leu Thr Tyr Ile Leu Met Gln Ala Arg Glu Ser Asp
 130          135          140
Leu Pro Glu Ala Ile His Val Leu Gly Phe Thr Glu Lys Gly Arg Gln
 145          150          155          160
His Leu Lys Ser Leu Lys Gly Gln Val Asn Leu Val Ser Arg Ile Gly
 165          170          175
Lys Glu Pro Trp Asp Ala Met Thr Gln Lys Val Asp Gln Ile Tyr Gln
 180          185          190
Leu Gly Lys Pro Ser Ile Ala Glu Gln Asn Phe Gly Arg Val Pro Ile
 195          200          205
Arg Ile Glu Thr Asn
 210

```

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

```

Met Leu Gly Ser Met Phe Val Gly Leu Leu Val Gly Phe Leu Ala Gly
 1           5           10           15

```

Ala Met Thr Asn Arg Gly Glu Arg Met Gly Cys Phe Gly Lys Met Phe
 20 25 30
 Leu Gly Trp Ile Gly Ala Phe Leu Gly His Leu Leu Phe Gly Thr Trp
 35 40 45
 Gly Pro Val Leu Ser Gly Thr Ala Ile Ile Pro Ala Val Leu Gly Ala
 50 55 60
 Met Ile Val Leu Ala Ile Phe Trp Arg Arg Gly Ser
 65 70 75

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

Met Arg Ser Ser Pro Ser Arg Glu Ile Gln Pro Arg Ser Trp Gly Ile
 1 5 10 15
 Thr Thr Val Tyr Val Thr His Asp Gln Glu Gly Ala Met Ala Ile Ser
 20 25 30
 Asp Gln Ile Ala Cys Tyr Glu Arg Trp Gly Asp Pro Thr Asn Arg Pro
 35 40 45
 Thr Lys Arg Thr Val Ser
 50

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of:
 - 5 (a) a polynucleotide having at least a 70% identity to a polynucleotide encoding a polypeptide comprising an amino acid sequence of selected from the group consisting of SEQ ID NO:224 through 477,
 - (b) a polynucleotide which is complementary to the polynucleotide of (a);
 - (c) a polynucleotide having at least a 70% identity to a polynucleotide encoding the
10 same mature polypeptide expressed by the a gene comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1 through 223 contained in the DNA of the deposited clone; and
 - (d) a polynucleotide comprising at least 15 sequential bases of the polynucleotide of (a), (b) or (c).
- 15 2. The polynucleotide of Claim 1 wherein the polynucleotide is DNA.
3. The polynucleotide of Claim 1 wherein the polynucleotide is RNA.
4. The polynucleotide of Claim 2 comprising the nucleic acid sequence set forth in SEQ ID NO:1.
5. The polynucleotide of Claim 2 comprising a nucleotide sequence selected from
20 the group consisting of SEQ ID NO:1 through 223.
6. The polynucleotide of Claim 2 which encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:224 through 477.
7. A vector comprising the polynucleotide of Claim 1.
8. A host cell comprising the vector of Claim 7.
- 25 9. A process for producing a polypeptide comprising: expressing from the host cell of Claim 8 a polypeptide encoded by said DNA.
10. A process for producing a novel polypeptide or fragment comprising culturing a host of claim 8 under conditions sufficient for the production of said polypeptide or fragment.
- 30 11. A polypeptide comprising an amino acid sequence which is at least 70% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:224 through 477.
12. A polypeptide comprising an amino acid selected from the group consisting of SEQ ID NO:224 through 477.

13. An antibody against the polypeptide of claim 11.
14. An antagonist which inhibits the activity or expression of the polypeptide of claim 11.
15. A method for the treatment of an individual in need of a Streptococcal polypeptide comprising: administering to the individual a therapeutically effective amount of the polypeptide of claim 11.
16. A method for the treatment of an individual having need to inhibit a bacterial polypeptide comprising: administering to the individual a therapeutically effective amount of the antagonist of Claim 14.
17. A process for diagnosing a disease related to expression or activity of the polypeptide of claim 11 in an individual comprising:
- (a) determining a nucleic acid sequence encoding said polypeptide, and/or
 - (b) analyzing for the presence or amount of said polypeptide in a sample derived from the individual.
18. A method for identifying compounds which interact with and inhibit or activate an activity of the polypeptide of claim 11 comprising:
- contacting a composition comprising the polypeptide with the compound to be screened under conditions to permit interaction between the compound and the polypeptide to assess the interaction of a compound, such interaction being associated with a second component capable of providing a detectable signal in response to the interaction of the polypeptide with the compound;
 - and determining whether the compound interacts with and activates or inhibits an activity of the polypeptide by detecting the presence or absence of a signal generated from the interaction of the compound with the polypeptide.
19. A method for inducing an immunological response in a mammal which comprises inoculating the mammal with Streptococcal polypeptide of claim 11, or a fragment or variant thereof, adequate to produce antibody and/or T cell immune response to protect said animal from disease.
20. A method of inducing immunological response in a mammal which comprises delivering a nucleic acid vector to direct expression of Streptococcal polypeptide of claim 11, or fragment or a variant thereof, for expressing said Streptococcal polypeptide, or a fragment or a variant thereof *in vivo* in order to induce an immunological response to produce antibody and/ or T cell immune response to protect said animal from disease.

21. An isolated Streptococcal polypeptide having one of the amino acid sequences of SEQ ID NO:224 through SEQ ID NO:234.
22. An isolated nucleic acid encoding one of the amino acid sequences of Claim 21 and nucleic acid sequences capable of hybridizing therewith under stringent conditions.
23. Recombinant vectors comprising the nucleic acid sequences of Claim 22 and host cells transformed or transfected therewith.
24. A method of identifying an antimicrobial compound comprising contacting candidate compounds with a polypeptide of Claim 21 and selecting those compounds capable of inhibiting the bioactivity of said polypeptide.
25. Antimicrobial compounds identified by the method of Claim 24.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/05306**A. CLASSIFICATION OF SUBJECT MATTER**

IPC(6) : Please See Extra Sheet.

US CL : 536/23.7; 435/6, 69.1, 252.3, 320.1; 530/324, 350; 514/12

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.7; 435/6, 69.1, 252.3, 320.1; 530/324, 350; 514/12

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X, P --- Y, P	WO 96/10647 A1 (FUSO PHARMACEUTICAL INDUSTRIES, LTD.) 11 April 1996, claim 2, pages 22-24.	1, 2, 7, 8, and 22 ----- 3, 6, 9-12, 15, 17, 21, and 23-25
Y	WATSON, J. D. et al. Recombinant DNA, Second Edition. New York: Scientific American Books, W.H. Freeman and Company, 1992, pages 73 and 74, see entire document.	1-3, 6-12, 15, 17, and 21-23
Y	KENNEL, D. E. Principles and Practices of Nucleic Acid Hybridization. Progress in Nucleic Acid Research Molecular Biology. 1971, Vol. 11, pages 259-301, see especially pages 259-262.	1-3, 6-12, 15, 17, and 21-23

☐ Further documents are listed in the continuation of Box C.☐ See patent family annex.

* Special categories of cited documents:	"T" later documents published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
E earlier document published on or after the international filing date	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Z" document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means	
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

10 JULY 1997

Date of mailing of the international search report

06 AUG 1997

Name and mailing address of the ISA/US
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/05306

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-3, 6-12, 15, 17, and 21-23 (SEQ ID NOs 224-233).

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/05306

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING (Continued):

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I. Claims 1-12, 15, 17, and 21-23, drawn to nucleic acids and polypeptides of specific sequence, vectors containing nucleic acids, methods of producing polypeptides, and methods of treatment using polypeptides.

Group II. Claims 13 and 19, drawn to antibodies against any of no fewer than 254 specific sequence polypeptides.

Group III. Claims 14 and 16, drawn to antagonists of undisclosed composition of the activity of no fewer than 254 specific sequence polypeptides.

Group IV. Claims 18 and 24, drawn to methods for screening for compounds that interact with no fewer than 254 specific sequence polypeptides.

Group V. Claim 20, drawn to a method of inducing an immunological response using a nucleic acid.

Group VI. Claim 25, drawn to compounds of undisclosed composition.

The inventions listed as Groups I-VI do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons. The nucleic acids, proteins, and methods of Group I are materially different from the antibodies of Group II, the compounds of Group III, and the compounds of Group VI and are not required to produce either the antibodies of Group II, which antibodies may be made with antigens other than those embraced by Group I. Additionally, the methods of Group I are not needed to produce the compounds of either one of Groups III or VI. The compositions and methods of Group I are not needed for the methods of either one of Groups IV or V. The antibodies of Group II are not needed for the methods of Groups IV or V and are materially different from the compounds of Groups III and VI. The antagonists of Group III are materially different from the compounds of Group VI because the antagonists and compounds have differing sites of action and/or binding. Neither are the compounds of either one of Groups III or VI needed to practice the methods of either one of Groups IV or V. The methods of Groups IV and V may be practiced independently of one another.

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack Unity of Invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows. Each of the 234 SEQ ID NOs listed is a separate species because there is no relationship between the species.

The species listed above do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, the species lack the same or corresponding special technical features for the following reasons. There is no relationship among the species.

For any Group applicant elects, a total of 10 (TEN) specified sequences will be searched and no more than 4 (FOUR) specified sequences will be searched for each additional fee paid.

The claims are deemed to correspond to the species listed above in the following manner: SEQ ID NOs 224-233 correspond to claims 1-3, 6-12, 15, 17, and 21-23.

A. CLASSIFICATION OF SUBJECT MATTER: IPC (6):

C12N 15/31, 15/11, 15/00; C12P 21/02; A61K 38/16, 39/09; C07K 14/195, 14/315

B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

MPSRCH OF: A-GENESEQ26, A-ISSUED, HIV-AA8, PIR50, SUIWW-PROT34, EMBL-NEW11, GENBANK97, GENBANK-NEW11, U-EMBL48_97, HIV-NA8, N-GENESEQ26, N-ISSUED, EST-STS, EST-STS-TWO, EST-STS-

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/05306

THREE. SEQ ID NOs 224-233.